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(12) **United States Patent**
Liao et al.(10) **Patent No.:** US 9,200,288 B2
(45) **Date of Patent:** Dec. 1, 2015(54) **PRODUCTION OF 1,4-BUTANEDIOL BY RECOMBINANT MICROORGANISMS**(75) Inventors: **James C. Liao**, Los Angeles, CA (US);
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C12N 15/52 (2006.01)
C12P 7/16 (2006.01)
C12P 7/18 (2006.01)(52) **U.S. Cl.**CPC **C12N 15/70** (2013.01); **C12N 15/52** (2013.01); **C12P 7/16** (2013.01); **C12P 7/18** (2013.01); **Y02E 50/10** (2013.01)(58) **Field of Classification Search**

None

See application file for complete search history.

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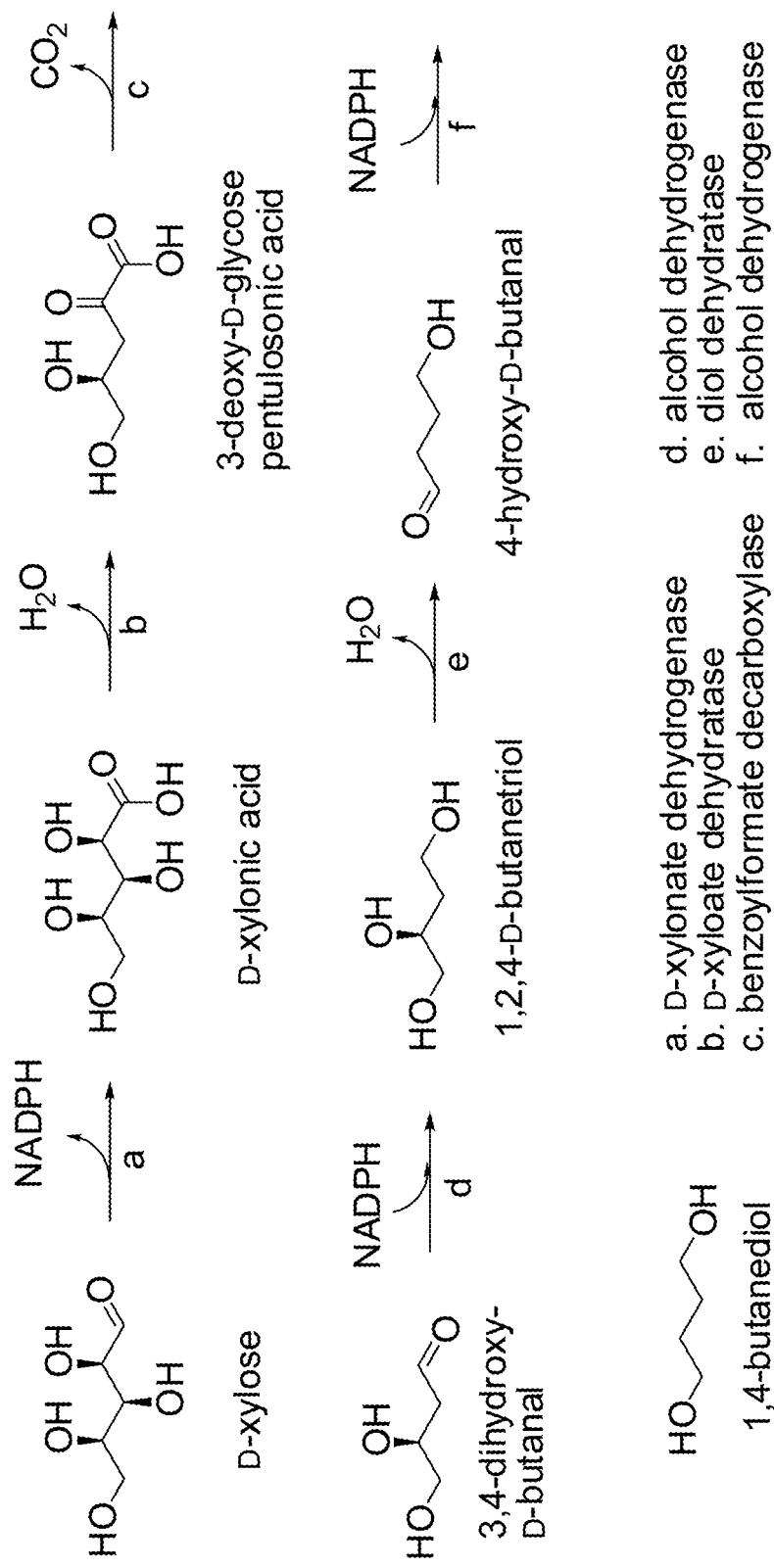
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(57) **ABSTRACT**

Provided herein are metabolically-modified microorganisms useful for producing 1,4-butanediol.

*Fig. 1.*

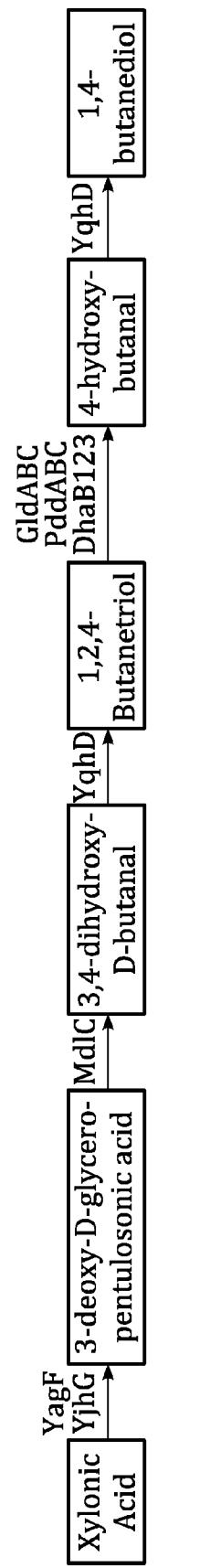


Fig. 2.

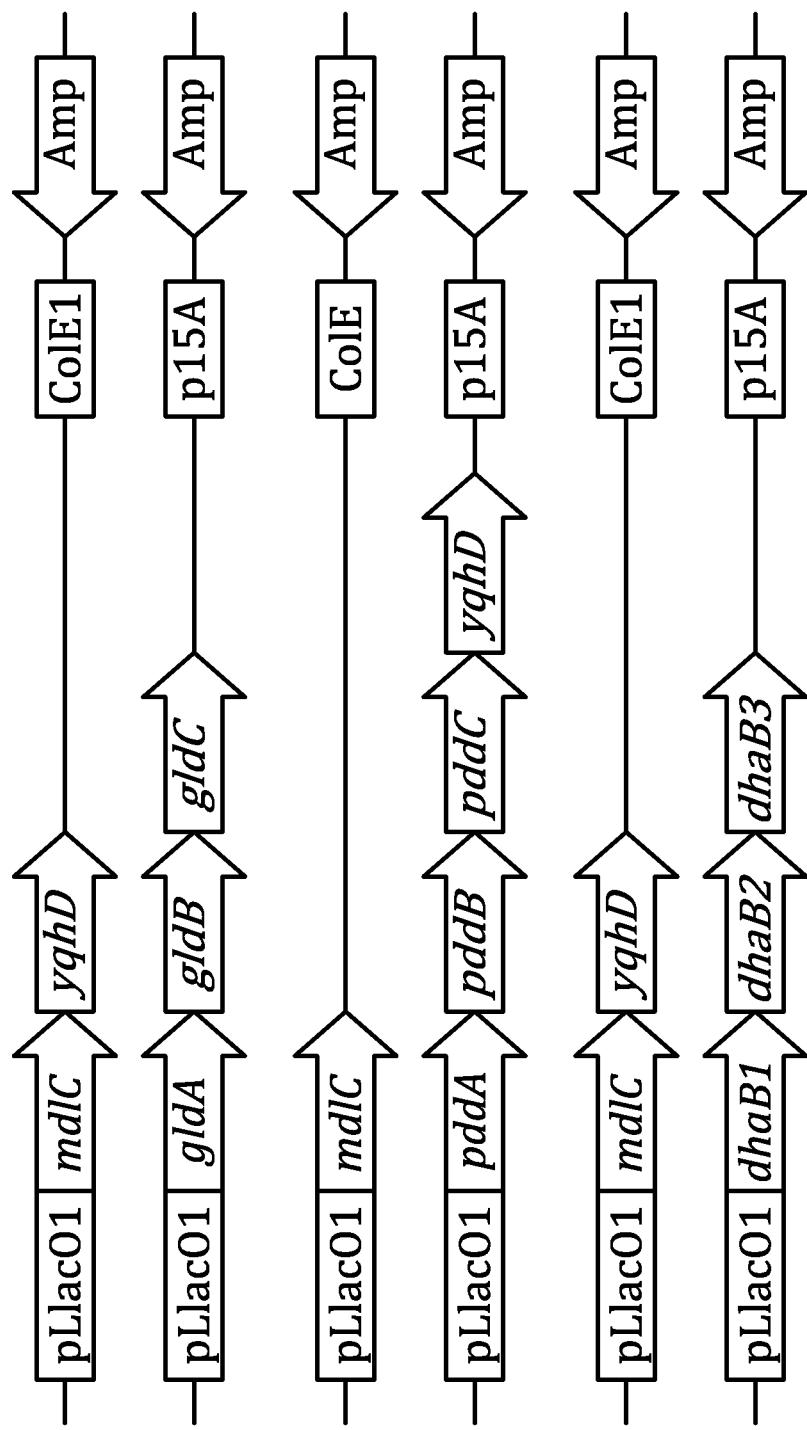
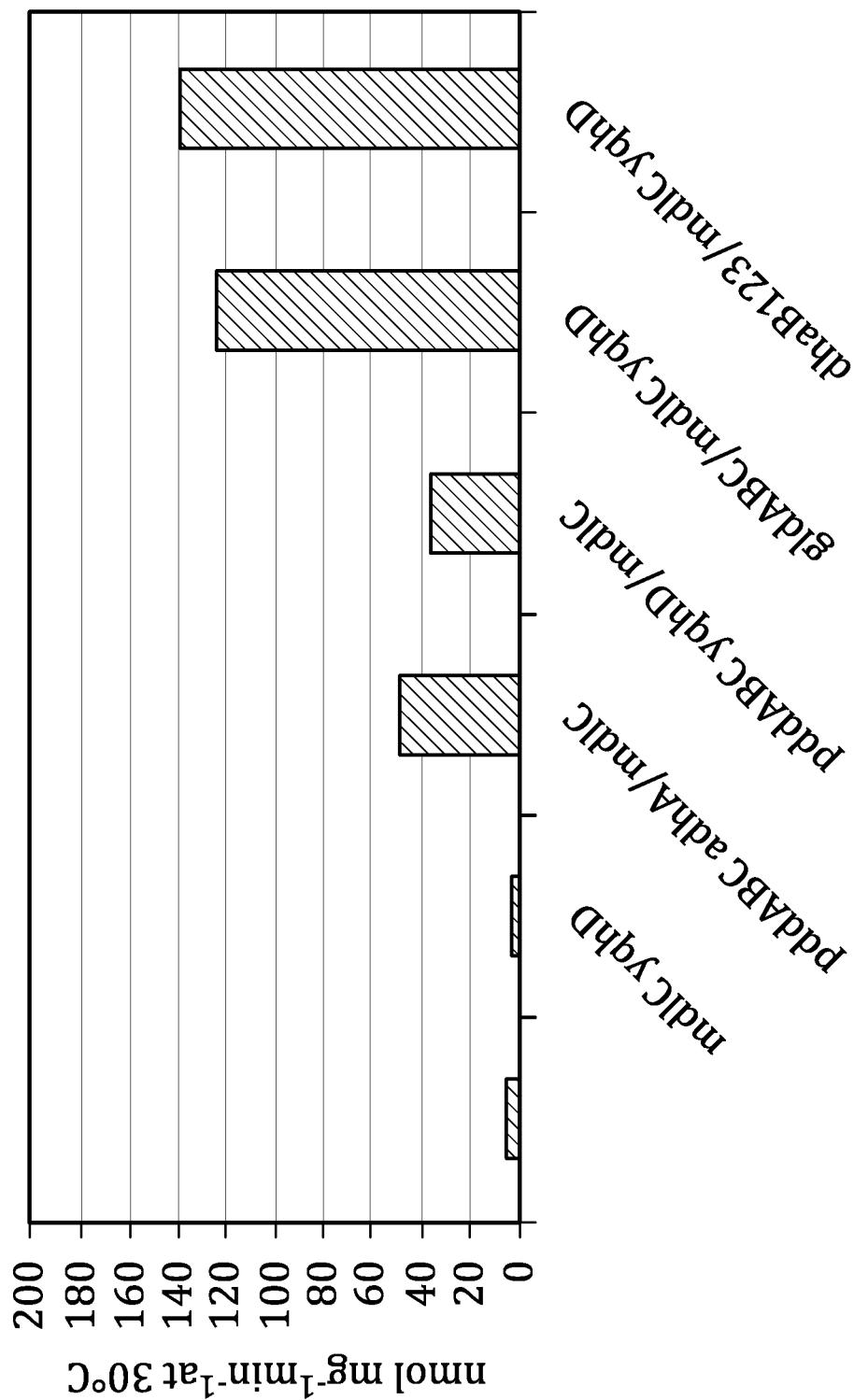


Fig. 3.



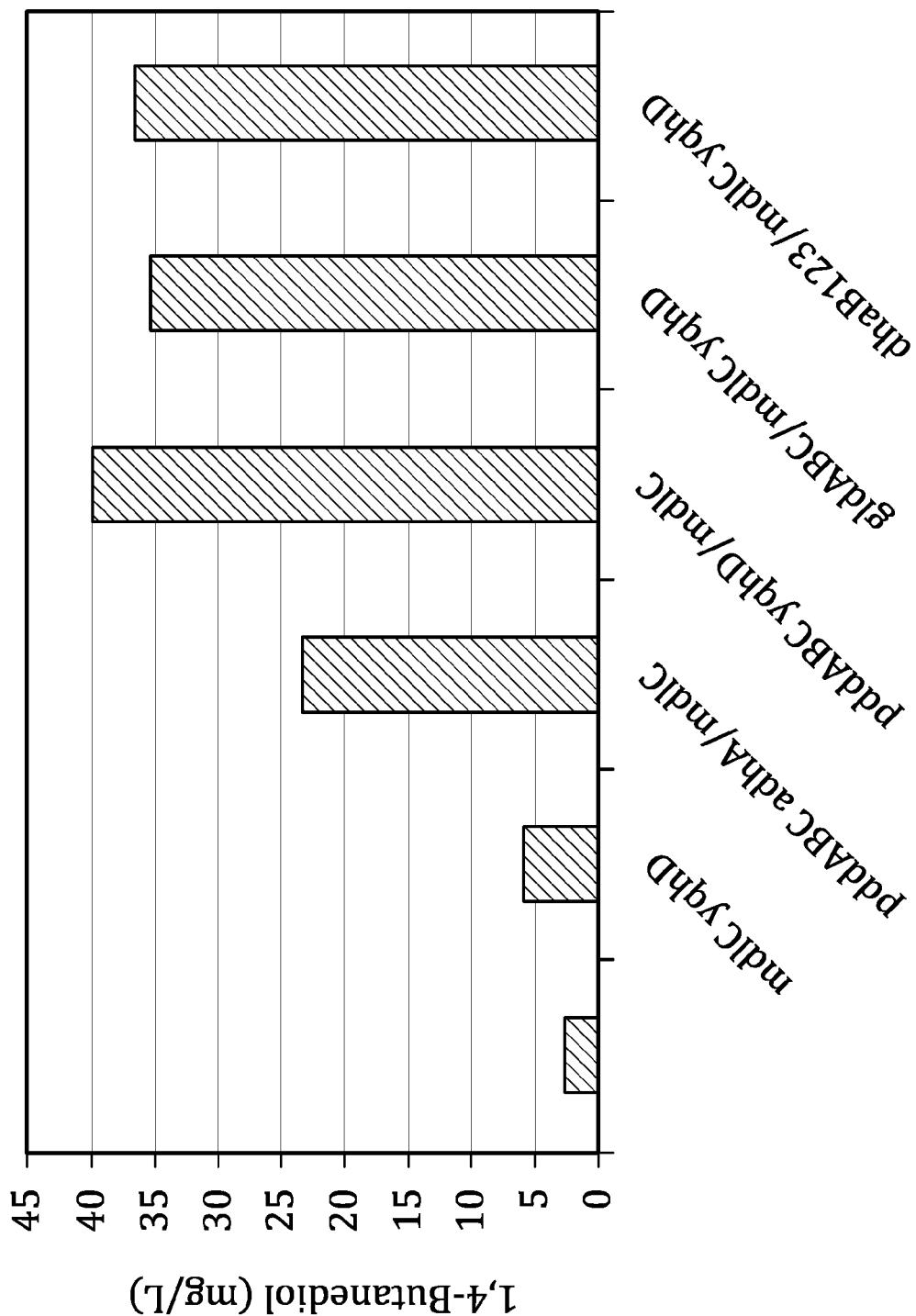


Fig. 5.

1**PRODUCTION OF 1,4-BUTANEDIOL BY RECOMBINANT MICROORGANISMS****CROSS-REFERENCE TO RELATED APPLICATION**

This application claims priority to U.S. Provisional Application Ser. No. 61/328,301, filed Apr. 27, 2010, the disclosure of which is incorporated herein by reference.

STATEMENT REGARDING SEQUENCE LISTING

The sequence listing associated with this application is provided in text format in lieu of a paper copy and is hereby incorporated by reference into the specification. The name of the text file containing the sequence listing is 36584_SEQ_FINAL.txt. The text file is 316 KB; was created on 27 Apr. 2011; and is being submitted via EFS-Web with the filing of the specification.

TECHNICAL FIELD

Metabolically-modified microorganisms and methods of producing such organisms are provided. Also provided are methods of producing 1,4-butanediol by contacting a suitable substrate with a metabolically-modified microorganism and enzymatic preparations there from.

BACKGROUND

1,4-Butanediol is an industrial solvent and is used in the manufacture of some types of plastics, elastic fibers, and polyurethanes. 1,4-Butanediol is also used for the synthesis of γ -butyrolactone (GBL). 1,4-Butanediol is also used for the production of the important solvents tetrahydrofuran and butyrolactone.

World production of 1,4-butanediol is about one million metric tons per year. Almost half of it is dehydrated to tetrahydrofuran to make fibers such as Spandex.

SUMMARY

The disclosure provides methods and recombinant microorganisms for the production of 1,4-butanediol.

In some embodiments, a recombinant microorganism is provided that produces 1,4-butanediol wherein the microorganism produces at least the following metabolic intermediates: a. xylonic acid; b. 3-deoxy-D-glycero-pentulose acid; c. 3,4-dihydroxy-D-butanal; d. 1,2,4-butanetriol; and e. 4-hydroxybutanal.

Also provided is a recombinant microorganism that over-expresses a xylonate dehydrogenase, a xylonate dehydratase, a decarboxylase, a first alcohol dehydrogenase, a diol dehydratase, and a second alcohol dehydrogenase, as compared to the parental microorganism.

Also provided is a method of producing a recombinant microorganism that converts xylose to 1,4-butanediol, the method comprising transforming a microorganism with one or more recombinant nucleic acid sequences encoding xylonate dehydrogenase activity, xylonate dehydratase activity, decarboxylase activity, a first alcohol dehydrogenase activity, diol dehydratase activity, and a second alcohol dehydrogenase activity.

Also provided is a method of producing 1,4-butanediol, comprising: a. providing a recombinant microorganism as disclosed herein; b. culturing the microorganism in the pres-

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ence of xylose under conditions suitable for the conversion of xylose to 1,4-butanediol; and c. isolating the 1,4-butanediol.

The disclosure also provides a recombinant microorganism or microorganism culture (e.g., a plurality of recombinant organisms with the same or different enzymes) that produces 1,4-butanediol comprising a recombinant metabolic pathway as set forth in FIG. 1. In one embodiment, the microorganism comprises expression of a non-natural polypeptide of the organism or over expression of an endogenous polypeptide of the organism wherein the polypeptide has an activity selected from the group consisting of xylose dehydrogenase; xylonate dehydratase; benzoylformate decarboxylase; alcohol dehydrogenase; diol dehydratase; and any combination thereof. In yet another embodiment, the microorganism comprises reduced or knocked-out expression of a polypeptide having an activity selected from the group consisting of: D-xylose isomerase (XylA); 2-keto acid aldolase (YagE and YjhH); 2-keto acid transaminase; 2-keto acid dehydrogenase; and any combination thereof.

The details of one or more embodiments of the disclosure are set forth in the accompanying drawings and the description below. Other features, objects, and advantages will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF THE DRAWINGS

The accompanying drawings, which are incorporated into and constitute a part of this specification, illustrate one or more embodiments of the disclosure and, together with the detailed description, serve to explain the principles and implementations of the invention.

FIG. 1 shows an exemplary metabolic pathway for the production of 1,4-butanediol.

FIG. 2 shows an exemplary metabolic pathway for the production of 1,4-butanediol. Xylose can be converted to 1,4-butanediol through the action of enzymes expressed by *E. coli* (YagF, YjhG, and each YqhD) and by the heterologous expression of enzymes from other microorganisms (MdIC, GldABC, PddABC, and DhaB124). Enzymes: Xdh (xylose dehydrogenase from *Caulobacter crescentus*), YagF and YjhG (xylonate dehydratases from *E. coli*), MdIC (benzoylformate decarboxylase from *Pseudomonas putida*), GldABC (diol dehydratase from *Klebsiella pneumoniae*), PddABC (diol dehydratase from *Klebsiella oxytoca*), and DhaB123 (diol dehydratase from *Clostridium butyricum*), YqhD (alcohol dehydrogenase from *E. coli*).

FIG. 3 shows exemplary plasmid pairs transformed into JCL16 for 1,4-butanediol production from D-xylonic acid.

FIG. 4 is a graph showing enzymatic activity of diol dehydratases PddABC, GldABC, and DhaB123. Diol dehydratase activity with 1,2,4-butanetriol was determined by a coupled reaction measuring the oxidation of NADPH in the presence of excess alcohol dehydrogenase.

FIG. 5 is a graph showing 1,4-butanediol production from D-xylonic acid. The JCL16 strains were grown in 20 ml with 20 g/L of D-xylonic acid at 30° C. for 24 hours.

DETAILED DESCRIPTION

As used herein and in the appended claims, the singular forms "a," "and," and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a polynucleotide" includes a plurality of such polynucleotides and reference to "the microorganism" includes reference to one or more microorganisms, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice of the disclosed methods and compositions, the exemplary methods, devices and materials are described herein.

Any publications discussed above and throughout the text are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior disclosure.

By "about" is meant a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight, or length that varies by as much as 30, 25, 20, 25, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1% to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight, or length.

The disclosure provides metabolically engineered microorganisms comprising biochemical pathways for the production of 1,4-butanediol from a suitable substrate. A metabolically engineered microorganism of the disclosure comprises one or more recombinant polynucleotides within the genome of the organism or external to the genome within the organism. The microorganism can comprise a reduction, disruption, or knockout of a gene found in the wild-type organism and/or introduction of a heterologous polynucleotide.

The disclosure also includes metabolically engineered biosynthetic pathways that utilize an organism's native pathways, in part, to provide metabolic intermediates for the production of 1,4-butanediol.

In one embodiment, the disclosure provides a recombinant microorganism comprising elevated expression of at least one target enzyme as compared to a parental microorganism or encodes an enzyme not found in the parental organism. In another or further embodiment, the microorganism comprises a reduction, disruption, or knockout of at least one gene encoding an enzyme that competes with a metabolite necessary for the production of a desired metabolic intermediate. The recombinant microorganism produces at least one metabolite involved in a biosynthetic pathway for the production of 1,4-butanediol. In general, the recombinant microorganism comprises at least one recombinant metabolic pathway that comprises a target enzyme and can further include a reduction in activity or expression of an enzyme in a competitive biosynthetic pathway. The pathway acts to modify a substrate or metabolic intermediate in the production of 1,4-butanediol. The target enzyme is encoded by, and expressed from, a polynucleotide derived from a suitable biological source. In some embodiments, the polynucleotide comprises a gene derived from a bacterial or yeast source and recombinantly engineered into the microorganism of the disclosure.

In some embodiments, a recombinant microorganism is provided that produces 1,4-butanediol wherein the microorganism produces at least the following metabolic intermediates: a. xylonic acid; b. 3-deoxy-D-glycero-pentulose acid; c. 3,4-dihydroxy-D-butanal; d. 1,2,4-butanetriol; and e. 4-hydroxybutanal.

In some embodiments, the microorganism over-expresses a xylonate dehydrogenase, a xylonate dehydratase, a decarboxylase, a first alcohol dehydrogenase, a diol dehydratase, and a second alcohol dehydrogenase, as compared to the parental microorganism.

The xylonate dehydrogenase may be endogenous or heterologous to the parental microorganism. The xylonate dehydrogenase may be derived from, e.g., *Burkholderia fungorum* or *Caulobacter crescentus*. In some embodiments, a xylonate

dehydrogenase comprises an amino acid sequence of either SEQ ID NO:2 or SEQ ID NO:4, or a conservative-substituted variant of or homologous polypeptide to either SEQ ID NO:2 or SEQ ID NO:4 having at least 70% identity to either SEQ ID NO:2 or SEQ ID NO:4 and having xylonate dehydrogenase activity. In some embodiments, the xylonate dehydrogenase comprises an amino acid sequence of either SEQ ID NO:11 or SEQ ID NO:12.

The xylonate dehydratase may be endogenous or heterologous to the parental microorganism. In some embodiments, the xylonate dehydratase is derived from *Escherichia coli*. The xylonate dehydratase may be an over-expressed endogenous *Escherichia coli* D-xylonate dehydratase associated with the *yagF* and *yjhG* loci in the *E. coli*. The xylonate dehydratase may be a heterologous D-xylonate dehydratase comprising the amino acid sequence of any one of SEQ ID NO:6, SEQ ID NO:8, or a conservative-substituted variant of or homologous polypeptide to SEQ ID NO:6 or SEQ ID NO:8 having at least 70% identity to SEQ ID NO:6 or SEQ ID NO:8 and having D-xylonate dehydratase activity.

In some embodiments, the decarboxylase is a benzoylformate decarboxylase. The benzoylformate decarboxylase may be endogenous or heterologous to the parental microorganism. In some embodiments, the benzoylformate decarboxylase is derived from *Pseudomonas pudica*. The benzoylformate decarboxylase may be a heterologous benzoylformate decarboxylase comprising the amino acid sequence of SEQ ID NO:9, or a conservative-substituted variant of or homologous polypeptide to SEQ ID NO:9 having at least 70% identity to SEQ ID NO:9 and having benzoylformate decarboxylase activity.

The first alcohol dehydrogenase or the second alcohol dehydrogenase may be endogenous or heterologous to the parental microorganism. In some embodiments, the first alcohol dehydrogenase or the second alcohol dehydrogenase is derived from *E. coli*. In some embodiments, the first alcohol dehydrogenase or the second alcohol dehydrogenase is a heterologous first alcohol dehydrogenase or a heterologous second alcohol dehydrogenase comprising the amino acid sequence of SEQ ID NO:10, or a conservative-substituted variant of or homologous polypeptide to SEQ ID NO:10 having at least 70% identity to SEQ ID NO:10 and having alcohol dehydrogenase activity. The first alcohol dehydrogenase may be the same as the second alcohol dehydrogenase. The first alcohol dehydrogenase may be different from the second alcohol dehydrogenase.

In some embodiments, the diol dehydratase is derived from *Listeria*, *Amycolatopsis*, *Klebsiella*, *Pseudomonas*, *Salmonella*, *Lactobacillus*, or *Yersinia*.

A recombinant microorganism may comprise decreased or knocked out expression of a polypeptide that produces a flux that competes with one or more metabolic intermediates. The polypeptide that produces a flux that competes with one or more metabolic intermediates can be selected from, e.g., a. a D-xylene isomerase; b. a 2-keto acid aldolase; c. a 2-keto acid transaminase; d. a 2-keto acid dehydrogenase; and any combination thereof.

Also provided is a recombinant microorganism that over-expresses a xylonate dehydrogenase, a xylonate dehydratase, a decarboxylase, a first alcohol dehydrogenase, a diol dehydratase, and a second alcohol dehydrogenase, as compared to the parental microorganism.

A recombinant microorganism may be, for example, an *Escherichia*, a *Corynebacterium*, a *Lactobacillus*, or a *Bacillus*.

Any recombinant microorganism disclosed herein may be comprised in a host cell, such as yeast or bacteria. In some

embodiments, the microorganism is comprised in a host cell selected from *Escherichia*, *Corynebacterium*, *Lactobacillus*, and *Bacillus*. In some embodiments, the microorganism is comprised in a host cell selected from *E. coli*, *Saccharomyces cerevisiae*, and *Pichia pastoris*.

Also provided is a method of producing a recombinant microorganism that converts xylose to 1,4-butanediol, the method comprising transforming a microorganism with one or more recombinant nucleic acid sequences encoding xylonate dehydrogenase activity, xylonate dehydratase activity, decarboxylase activity, a first alcohol dehydrogenase activity, diol dehydratase activity, and a second alcohol dehydrogenase activity.

Also provided is a method of producing 1,4-butanediol, comprising: a. providing a recombinant microorganism as disclosed herein; b. culturing the microorganism in the presence of xylose under conditions suitable for the conversion of xylose to 1,4-butanediol; and c. isolating the 1,4-butanediol.

As used herein, the term “metabolically engineered” or “metabolic engineering” involves rational pathway design and assembly of biosynthetic genes, genes associated with operons, and control elements of such polynucleotides, for the production of a desired metabolite, such as a D-xylonic acid, 3,4-dihydroxy-D-butanal, and the like as set forth in FIG. 1 in a microorganism. “Metabolically engineered” can further include optimization of metabolic flux by regulation and optimization of transcription, translation, protein stability, and protein functionality using genetic engineering and appropriate culture conditions including the reduction of, disruption, or knocking out of, a competing metabolic pathway that competes with an intermediate leading to a desired pathway. A biosynthetic gene can be heterologous to the host microorganism, either by virtue of being foreign to the host, or being modified by mutagenesis, recombination, and/or association with a heterologous expression control sequence in an endogenous host cell. In one embodiment, where the polynucleotide is xenogenetic to the host organism, the polynucleotide can be codon optimized.

The term “biosynthetic pathway”, also referred to as “metabolic pathway”, refers to a set of anabolic or catabolic biochemical reactions for converting (transmuting) one chemical species into another. Gene products belong to the same “metabolic pathway” if they, in parallel or in series, act on the same substrate, produce the same product, or act on or produce a metabolic intermediate (i.e., metabolite) between the same substrate and metabolite end product.

The term “substrate” or “suitable substrate” refers to any substance or compound that is converted or meant to be converted into another compound by the action of an enzyme. The term includes not only a single compound, but also combinations of compounds, such as solutions, mixtures and other materials which contain at least one substrate, or derivatives thereof. Further, the term “substrate” encompasses not only compounds that provide a carbon source suitable for use as a starting material, such as any biomass derived sugar, but also intermediate and end product metabolites used in a pathway associated with a metabolically engineered microorganism as described herein. A “biomass derived sugar” includes, but is not limited to, molecules such as glucose, sucrose, mannose, xylose, and arabinose. The term biomass derived sugar encompasses suitable carbon substrates ordinarily used by microorganisms in either D or L form.

Recombinant microorganisms provided herein can express a plurality of target enzymes involved in pathways for the production of 1,4-butanediol from using a suitable carbon substrate.

Accordingly, metabolically “engineered” or “modified” microorganisms are produced via the introduction of genetic material into a host or parental microorganism of choice thereby modifying or altering the cellular physiology and biochemistry of the microorganism. Through the introduction of genetic material the parental microorganism acquires new properties, e.g., the ability to produce a new, or greater quantities of, an intracellular metabolite. In an illustrative embodiment, the introduction of genetic material into a parental microorganism results in a new or modified ability to produce 1,4-butanediol. The genetic material introduced into the parental microorganism contains gene(s), or parts of genes, coding for one or more of the enzymes involved in a biosynthetic pathway for the production of 1,4-butanediol and can also include additional elements for the expression and/or regulation of expression of these genes, e.g., promoter sequences.

An engineered or modified microorganism can also include in the alternative, or in addition to, the introduction of a genetic material into a host or parental microorganism, the disruption, deletion, or knocking out of a gene or polynucleotide to alter the cellular physiology and biochemistry of the microorganism. Through the reduction, disruption, or knocking out of a gene or polynucleotide, the microorganism acquires new or improved properties (e.g., the ability to produce a new or greater quantities of an intracellular metabolite, improve the flux of a metabolite down a desired pathway, and/or reduce the production of undesirable by-products).

The disclosure demonstrates that the expression of one or more heterologous polynucleotide(s) or over-expression of one or more heterologous polynucleotide(s) encoding i) a polypeptide having xylose (xylonate) dehydrogenase activity and ii) a polypeptide having xylonate dehydratase activity, iii) a polypeptide having benzoylformate decarboxylase activity, iv) a polypeptide having alcohol dehydrogenase activity, and v) a polypeptide having diol dehydratase activity, will produce 1,4-butanediol.

For example, the disclosure demonstrates that with (i) over-expression or heterologous expression of a D-xylose dehydrogenase comprising the amino acid sequence of any one of SEQ ID NO:2 or SEQ ID NO:4 (See Tables 1 and 2), or a conservative-substituted variant of or homologous polypeptide to SEQ ID NO:2 or SEQ ID NO:4 having at least 70 to 99% identity to SEQ ID NO:2 or 4 and having D-xylose dehydrogenase activity (such as a xylose dehydrogenase derived from *Haloarcula marismortui*, *Burkholderia fujorum* LB400, *Haloferax volcanii* DS2, (see, e.g., GenBank Accession Nos. AAW78223 (SEQ ID NO:11), RBU11704 (SEQ ID NO:2), and YP_003533786 (SEQ ID NO:12), respectively, the sequence associated with the accession number is incorporated herein by reference); (ii) over-expression of the endogenous *E. coli* D-xylonate dehydratase associated with the *yagF* and *yjhG* loci in the *E. coli* or the heterologous expression of a D-xylonic acid dehydratase comprising the amino acid sequence of any one of SEQ ID NO:6 (See Table 3), SEQ ID NO:8 (See Table 4), or a conservative-substituted variant of or homologous polypeptide to SEQ ID NO:6 or SEQ ID NO:8 having at least 60% to 99% identity to SEQ ID NO:6 or 8 and having D-xylonate dehydratase activity; (iii) over-expression or heterologous expression of a decarboxylase such as, for example, a benzoylformate decarboxylase from *Pseudomonas putida* comprising an amino acid sequence as set forth in SEQ ID NO:9 (see also Table 5) and sequences having at least 60 to 99% identity to a sequence set forth in SEQ ID NO:9 or a homology or ortholog set forth in Table 5 and having decarboxylase activity; (iv) over expression or heterologous expression of an alcohol dehydrogenase (e.g., an AdhP alcohol dehydrogenase from *E.*

coli) having, for example, an amino acid sequence as set forth in SEQ ID NO:10 (see also Table 6) and sequences having at least 60 to 99% identity to a sequence set forth in SEQ ID NO:10 or a homology or ortholog set forth in Table 6 and

having alcohol dehydrogenase activity; and (v) over expression or heterologous expression of a diol dehydratase (also known as "butanediol dehydratase" or "propanediol dehydratase"), 1,4-butanediol will be produced.

TABLE 1

Coding sequence for *Burkholderia fungorum* LB400 RBU11704 xylose dehydrogenase. SEQ ID NO: 1 and SEQ ID NO: 2

atg tat ttg ttg tca tac ccg gaa cag gtg gac tat ccg atg tcg tac	48
Met Tyr Leu Leu Ser Tyr Pro Glu Gln Val Asp Tyr Pro Met Ser Tyr	
1 5 10 15	
gca atc tat ccc agc ctc tca ggc aaa acg gtt gtc atc acc ggc ggc	96
Ala Ile Tyr Pro Ser Leu Ser Gly Lys Thr Val Val Ile Thr Gly Gly	
20 25 30	
ggc agc ggc atc ggc gcc gcg atg gtc gaa gct ttc gcc cgg cag ggc	144
Gly Ser Gly Ile Gly Ala Ala Met Val Glu Ala Phe Ala Arg Gln Gly	
35 40 45	
gcg cga gtt ttc ttc ctc gac gtc gct gag gac gat tcg ctg gcg ttg	192
Ala Arg Val Phe Phe Leu Asp Val Ala Glu Asp Asp Ser Leu Ala Leu	
50 55 60	
cag caa tcg ctg agc gac gcg cct cac ccg ccg ttg ttc cgc cgc tgc	240
Gln Gln Ser Leu Ser Asp Ala Pro His Pro Pro Leu Phe Arg Arg Cys	
65 70 75 80	
gat ctg cgc agc gtc gat gcg atc cac agt gcg ttt gcc ggg atc gtc	288
Asp Leu Arg Ser Val Asp Ala Ile His Ser Ala Phe Ala Gly Ile Val	
85 90 95	
gag atc gcc ggg ccg atc gag gta ctc gtc aac aac gct ggc aac gac	336
Glu Ile Ala Gly Pro Ile Glu Val Leu Val Asn Asn Ala Gly Asn Asp	
100 105 110	
gac cgg cat gaa gtc gac gcc atc acg ccg gcc tat tgg gac gag cgc	384
Asp Arg His Glu Val Asp Ala Ile Thr Pro Ala Tyr Trp Asp Glu Arg	
115 120 125	
atg gcc gtg aac ctg cgg cac cag ttc ttc tgc gcg cag gcc gca gcg	432
Met Ala Val Asn Leu Arg His Gln Phe Phe Cys Ala Gln Ala Ala Ala	
130 135 140	
gcc ggc atg cgc aag atc ggg cgc ggc gtg atc ctg aat ctt ggc tgc	480
Ala Gly Met Arg Lys Ile Gly Arg Gly Val Ile Leu Asn Leu Gly Ser	
145 150 155 160	
gtt tcc tgg cac ctc gcg ttg ccg aac ctc gcg atc tac atg agc gcg	528
Val Ser Trp His Leu Ala Leu Pro Asn Leu Ala Ile Tyr Met Ser Ala	
165 170 175	
aag gcc ggt atc gaa ggg ctg acc ccg ggc ctc gcg cgc gat ctc ggc	576
Lys Ala Gly Ile Glu Gly Leu Thr Arg Gly Leu Ala Arg Asp Leu Gly	
180 185 190	
gcc gcc ggc atc cgc gtg aac tgc att att ccc ggc gcg gtg cgg act	624
Ala Ala Gly Ile Arg Val Asn Cys Ile Ile Pro Gly Ala Val Arg Thr	
195 200 205	
ccc cgt cag atg cag ctc tgg cag tcg ccc gag agc gaa ggc aag ctc	672
Pro Arg Gln Met Gln Leu Trp Gln Ser Pro Glu Ser Glu Ala Lys Leu	
210 215 220	
gtc gcc agc caa tgt ctg cgt ttg cgt atc gaa cct gag cat gtc gcg	720
Val Ala Ser Gln Cys Leu Arg Leu Arg Ile Glu Pro Glu His Val Ala	
225 230 235 240	
cgc atg gcg ttg ttt ctt gcg tcc gac gat ggc tcg cgt tgc tca ggg	768
Arg Met Ala Leu Phe Leu Ala Ser Asp Asp Ala Ser Arg Cys Ser Gly	
245 250 255	
cgg gat tat ttc gtc gac gcc ggg tgg tac gga gaa tga	807
Arg Asp Tyr Phe Val Asp Ala Gly Trp Tyr Gly Glu	
260 265	

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9**10**

TABLE 2

Coding sequences for *Caulobacter crescentus* CB15 RC001012 xylose dehydrogenase. SEQ ID NO: 3 and SEQ ID NO: 4:

atg tcc tca gcc atc tat ccc aac ctg aag ggc aag cgc gtc gtc atc 48
Met Ser Ala Ile Tyr Pro Ser Leu Lys Gly Lys Arg Val Val Ile
1 5 10 15

acc ggc ggc ggc tcg ggc atc ggg ggc ctc acc gcc ggc ttc gcc 96
Thr Gly Gly Ser Gly Ile Gly Ala Gly Leu Thr Ala Gly Phe Ala
20 25 30

cgt cag ggc gcg gag gtg atc ttc ctc gac atc gcc gac gag gac tcc 144
Arg Gln Gly Ala Glu Val Ile Phe Leu Asp Ile Ala Asp Glu Asp Ser
35 40 45

agg gct ctt gag gcc gag ctg gcc tcg ccc atc ccg ccg gtc tac 192
Arg Ala Leu Glu Ala Glu Leu Ala Gly Ser Pro Ile Pro Val Tyr
50 55 60

aag cgc tgc gac ctg atg aac ctc gag ggc atc aag ggc gtc ttc gcc 240
Lys Arg Cys Asp Leu Met Asn Leu Glu Ala Ile Lys Ala Val Phe Ala
65 70 75 80

gag atc ggc gac gtc gac gtg ctg gtc aac aac gcc ggc aat gac gac 288
Glu Ile Gly Asp Val Asp Val Leu Val Asn Asn Ala Gly Asn Asp Asp
85 90 95

cgc cac aag ctg gcc gac gtg acc ggc gcc tat tgg gac gag cgg atc 336
Arg His Lys Leu Ala Asp Val Thr Gly Ala Tyr Trp Asp Glu Arg Ile
100 105 110

aac gtc aac ctg cgc cac atg ctg ttc tgc acc cag gcc gtc gcg ccg 384
Asn Val Asn Leu Arg His Met Leu Phe Cys Thr Gln Ala Val Ala Pro
115 120 125

ggc atg aag aag cgt ggc ggc ggg gcg gtg atc aac ttc ggt tcg atc 432
Gly Met Lys Lys Arg Gly Gly Ala Val Ile Asn Phe Gly Ser Ile
130 135 140

agc tgg cac ctg ggg ctt gag gac ctc gtc ctc tac gaa acc gcc aag 480
Ser Trp His Leu Gly Leu Glu Asp Leu Val Leu Tyr Glu Thr Ala Lys
145 150 155 160

gcc ggc atc gaa ggc atg acc cgc gcg ctg gcc ccg gag ctg ggt ccc 528
Ala Gly Ile Glu Gly Met Thr Arg Ala Leu Ala Arg Glu Leu Gly Pro
165 170 175

gac gac atc cgc gtc acc tgc gtg ccg ggc aac gtc aag acc aag 576
Asp Asp Ile Arg Val Thr Cys Val Val Pro Gly Asn Val Lys Thr Lys
180 185 190

cgc cag gag aag tgg tac acg ccc gaa ggc gag gcc cag atc gtg gcg 624
Arg Gln Glu Lys Trp Tyr Thr Pro Glu Gly Glu Ala Gln Ile Val Ala
195 200 205

gcc caa tgc ctg aag ggc cgc atc gtc ccg gag aac gtc gcc gcg ctg 672
Ala Gln Cys Leu Lys Gly Arg Ile Val Pro Glu Asn Val Ala Ala Leu
210 215 220

gtg ctg ttc ctg gcc tcg gat gac gcg tcg ctc tgc acc ggc cac gaa 720
Val Leu Phe Leu Ala Ser Asp Asp Ala Ser Leu Cys Thr Gly His Glu
225 230 235 240

tac tgg atc gac gcc ggc tgg cgt tga 747
Tyr Trp Ile Asp Ala Gly Trp Arg
245

TABLE 3

Coding sequence for *Escherichia coli* yagF xylonate dehydratase.
SEQ ID NO: 5 and SEQ ID NO: 6.

atg acc att gag aaa att ttc acc ccg cag gac gac gcg ttt tat gcg 48
Met Thr Ile Glu Lys Ile Phe Thr Pro Gln Asp Asp Ala Phe Tyr Ala
1 5 10 15

gtg atc acc cac gcg gcg ggg ccg cag ggc gct ctg ccg acc ccg 96

TABLE 3-continued

Coding sequence for <i>Escherichia coli</i> yagF xylonate dehydratase.			
SEQ ID NO: 5 and SEQ ID NO: 6.			
Val Ile Thr His Ala Ala Gly Pro Gln Gly Ala Leu Pro Leu Thr Pro			
20	25	30	
cag atg ctg atg gaa tct ccc agc ggc aac ctg ttc ggc atg acg cag			144
Gln Met Leu Met Glu Ser Pro Ser Gly Asn Leu Phe Gly Met Thr Gln			
35	40	45	
aac gcc ggg atg ggc tgg gac gcc aac aag ctc acc ggc aaa gag gtg			192
Asn Ala Gly Met Gly Trp Asp Ala Asn Lys Leu Thr Gly Lys Glu Val			
50	55	60	
ctg att atc ggc act cag ggc ggc atc cgc gcc gga gac gga cgc cca			240
Leu Ile Ile Gly Thr Gln Gly Ile Arg Ala Gly Asp Gly Arg Pro			
65	70	75	80
atc gcg ctg ggc tac cac acc ggg cat tgg gag atc ggc atg cag atg			288
Ile Ala Leu Gly Tyr His Thr Gly His Trp Glu Ile Gly Met Gln Met			
85	90	95	
cag gcg gcg aag gag atc acc cgc aat ggc ggg atc ccg ttc gcg			336
Gln Ala Ala Lys Glu Ile Thr Arg Asn Gly Ile Pro Phe Ala			
100	105	110	
gcc ttc gtc agc gat ccg tgc gac ggg cgc tcg cag ggc acg cac ggt			384
Ala Phe Val Ser Asp Pro Cys Asp Gly Arg Ser Gln Gly Thr His Gly			
115	120	125	
atg ttc gat tcc ctg ccg tac cgc aac gac gcg gcg atc gtg ttt cgc			432
Met Phe Asp Ser Leu Pro Tyr Arg Asn Asp Ala Ala Ile Val Phe Arg			
130	135	140	
cgc ctg atc cgc tcc ctg ccg acg cgg cgg gcg gtg atc ggc gta gcg			480
Arg Leu Ile Arg Ser Leu Pro Thr Arg Arg Ala Val Ile Gly Val Ala			
145	150	155	160
acc tgc gat aaa ggg ctg ccc gcc acc atg att gcg ctg gcc gcg atg			528
Thr Cys Asp Lys Glu Leu Pro Ala Thr Met Ile Ala Leu Ala Ala Met			
165	170	175	
cac gac ctg ccg act att ctg gtg ccg ggc ggg gcg acg ctg ccg ccg			576
His Asp Leu Pro Thr Ile Leu Val Pro Gly Gly Ala Thr Leu Pro Pro			
180	185	190	
acc gtc ggg gaa gac gcg ggc aag gtg cag acc atc ggc gcg cgt ttc			624
Thr Val Gly Glu Asp Ala Gly Lys Val Gln Thr Ile Gly Ala Arg Phe			
195	200	205	
gcc aac cac gaa ctc tcc ctg cag gag gcc gcc gaa ctg ggc tgt cgc			672
Ala Asn His Glu Leu Ser Leu Gln Glu Ala Ala Glu Leu Gly Cys Arg			
210	215	220	
gcc tgc gcc tcg ccg ggc ggc ggg tgt cag ttc ctc ggc acg gcg ggc			720
Ala Cys Ala Ser Pro Gly Gly Cys Gln Phe Leu Gly Thr Ala Gly			
225	230	235	240
acc tcg cag gtg gtc gcg gag gcg ctg ggt ctg gcg ctg ccg cac tcc			768
Thr Ser Gln Val Val Ala Glu Ala Leu Gly Leu Ala Leu Pro His Ser			
245	250	255	
gcg ctg gcg ccg tcc ggg cag gcg gtg tgg ctg gag atc gcc cgc cag			816
Ala Leu Ala Pro Ser Gly Gln Ala Val Trp Leu Glu Ile Ala Arg Gln			
260	265	270	
tcg gcg cgc gtc agc gag ctg gat agc cgc ggc atc acc acg cgg			864
Ser Ala Arg Ala Val Ser Glu Leu Asp Ser Arg Gly Ile Thr Thr Arg			
275	280	285	
gat atc ctc tcc gat aaa gcc atc gaa aac gcg atg gtg atc cac gcg			912
Asp Ile Leu Ser Asp Lys Ala Ile Glu Asn Ala Met Val Ile His Ala			
290	295	300	
gcg ttc ggc ggc tcc acc aat tta ctg ctg cac att ccg gcc atc gcc			960
Ala Phe Gly Gly Ser Thr Asn Leu Leu His Ile Pro Ala Ile Ala			
305	310	315	320
cac gcg gcg ggc tgc acg atc ccg gac gtt gag cac tgg acg cgc atc			1008
His Ala Ala Gly Cys Thr Ile Pro Asp Val Glu His Trp Thr Arg Ile			

TABLE 3-continued

Coding sequence for <i>Escherichia coli</i> yagF xylonate dehydratase.		
SEQ ID NO: 5 and SEQ ID NO: 6.		
325	330	335
aac cgt aaa gtg ccg cgt ctg gtg agc gtg ctg ccc aac ggc ccg gac Asn Arg Lys Val Pro Arg Leu Val Ser Val Leu Pro Asn Gly Pro Asp 340 345 350		1056
tat cac ccg acc gtg cgc gcc ttc ctc gcg ggc gtg ccg gag gtg Tyr His Pro Thr Val Arg Ala Phe Leu Ala Gly Gly Val Pro Glu Val 355 360 365		1104
atg ctc cac ctg cgc gac ctc ggc ctg ctg cat ctg gac gcc atg acc Met Leu His Leu Arg Asp Leu Gly Leu Leu His Leu Asp Ala Met Thr 370 375 380		1152
gtg acc ggc cag acg gtg ggc gag aac ctt gaa tgg tgg cag ggc tcc Val Thr Gly Gln Thr Val Gly Glu Asn Leu Glu Trp Trp Gln Ala Ser 385 390 395 400		1200
gag cgc cgg cgc ttc cgc cag tgc ctg cgc gag cag gac ggc gta Glu Arg Arg Ala Arg Phe Arg Gln Cys Leu Arg Glu Gln Asp Gly Val 405 410 415		1248
gag ccg gat gac gtg atc ctg ccg gag aag gca aaa gcg aaa ggg Glu Pro Asp Asp Val Ile Leu Pro Pro Glu Lys Ala Lys Ala Lys Gly 420 425 430		1296
ctg acc tcg acg gtc tgc ttc ccg acg ggc aac atc gct ccg gaa ggt Leu Thr Ser Thr Val Cys Phe Pro Thr Gly Asn Ile Ala Pro Glu Gly 435 440 445		1344
tcg gtg atc aag gcc acg gcg atc gac ccg tgc gtg gtc gaa gat Ser Val Ile Lys Ala Thr Ala Ile Asp Pro Ser Val Val Gly Glu Asp 450 455 460		1392
ggc gta tac cac cac acc ggc cgg gtg cgg gtg ttt gtc tcg gaa gcg Gly Val Tyr His His Thr Gly Arg Val Arg Val Phe Val Ser Glu Ala 465 470 475 480		1440
cag gcg atc aag gcg atc aag cgg gaa gag att gtg cag ggc gat atc Gln Ala Ile Lys Ala Ile Lys Arg Glu Glu Ile Val Gln Gly Asp Ile 485 490 495		1488
atg gtg gtg atc ggc ggg ccg tcc ggc acc ggc atg gaa gag acc Met Val Val Ile Gly Gly Pro Ser Gly Thr Gly Met Glu Glu Thr 500 505 510		1536
tac cag ctc acc tcc gcg cta aag cat atc tcg tgg ggc aag acg gtg Tyr Gln Leu Thr Ser Ala Leu Lys His Ile Ser Trp Gly Lys Thr Val 515 520 525		1584
tcg ctc atc acc gat gcg cgc ttc tcg ggc gtg tcg acg ggc gcc tgc Ser Leu Ile Thr Asp Ala Arg Phe Ser Gly Val Ser Thr Gly Ala Cys 530 535 540		1632
ttc ggc cac gtg tcg ccg gag gcg ctg gcg ggc ggg ccg att ggc aag Phe Gly His Val Ser Pro Glu Ala Leu Ala Gly Gly Pro Ile Gly Lys 545 550 555 560		1680
ctg cgc gat aac gac atc atc gag att gcc gtg gat cgt ctg acg tta Leu Arg Asp Asn Asp Ile Ile Glu Ile Ala Val Asp Arg Leu Thr Leu 565 570 575		1728
act ggc agc gtg aac ttc atc ggc acc gcg gac aac ccg ctg acg ccg Thr Gly Ser Val Asn Phe Ile Gly Thr Ala Asp Asn Pro Leu Thr Pro 580 585 590		1776
gaa gag ggc gcg cgc gag ctg gcg cgg cgg cag acg cac ccg gac ctg Glu Glu Gly Ala Arg Glu Leu Ala Arg Arg Gln Thr His Pro Asp Leu 595 600 605		1824
cac gcc cac gac ttt ttg ccg gac acc cgg ctg tgg gcg gca ctg His Ala His Asp Phe Leu Pro Asp Asp Thr Arg Leu Trp Ala Ala Leu 610 615 620		1872
cag tcg gtg agc ggc ggc acc tgg aaa ggc tgt att tat gac acc gat Gln Ser Val Ser Gly Gly Thr Trp Lys Gly Cys Ile Tyr Asp Thr Asp 625 630 635 640		1920

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15

TABLE 3-continued

Coding sequence for *Escherichia coli* yagF xylonate dehydratase.
SEQ ID NO: 5 and SEQ ID NO: 6.

aaa att atc gag gta att aac gcc ggt aaa aaa gcg ctc gga att taa	1968
Lys Ile Ile Glu Val Ile Asn Ala Gly Lys Lys Ala Leu Gly Ile	
645	650
	655

16

TABLE 4

Coding sequences for *E. coli* yjhG xylonate dehydratase.
SEQ ID NO: 7 and SEQ ID NO: 8

atg tct gtt cgc aat att ttt gct gac gag agc cac gat att tac acc	48
Met Ser Val Arg Asn Ile Phe Ala Asp Glu Ser His Asp Ile Tyr Thr	
1	5
	10
	15

gtc aga acg cac gcc gat ggc ccg gac gga ctc cca tta acc gca	96
Val Arg Thr His Ala Asp Gly Pro Asp Gly Glu Leu Pro Leu Thr Ala	
20	25
	30

gag atg ctt atc aac cgc ccg agc ggg gat ctg ttc ggt atg acc atg	144
Glu Met Leu Ile Asn Arg Pro Ser Gly Asp Leu Phe Gly Met Thr Met	
35	40
	45

aat gcc gga atg ggt tgg tct ccg gac ctg gat cgg gac ggt att	192
Asn Ala Gly Met Gly Trp Ser Pro Asp Glu Leu Asp Arg Asp Gly Ile	
50	55
	60

tta ctg ctc agt aca ctc ggt ggc tta cgc ggc gca gac ggt aaa ccc	240
Leu Leu Leu Ser Thr Leu Gly Gly Leu Arg Ala Asp Gly Lys Pro	
65	70
	75
	80

gtg gcg ctg gcg ttg cac cag ggg cat tac gaa ctg gac atc cag atg	288
Val Ala Leu Ala His Gln Gly His Tyr Glu Leu Asp Ile Gln Met	
85	90
	95

aaa gcg gcg gcc gag gtt att aaa gcc aac cat gcc ctg ccc tat gcc	336
Lys Ala Ala Ala Glu Val Ile Lys Ala Asn His Ala Leu Pro Tyr Ala	
100	105
	110

gtg tac gtc tcc gat cct tgt gac ggg cgt act cag ggt aca acg ggg	384
Val Tyr Val Ser Asp Pro Cys Asp Gly Arg Thr Gln Gly Thr Thr Gly	
115	120
	125

atg ttt gat tcg cta cca tac cga aat gac gca tcg atg gta atg cgc	432
Met Phe Asp Ser Leu Pro Tyr Arg Asn Asp Ala Ser Met Val Met Arg	
130	135
	140

cgc ctt att cgc tct ctg ccc gac gcg aaa gca gtt att ggt gtg gcg	480
Arg Leu Ile Arg Ser Leu Pro Asp Ala Lys Ala Val Ile Gly Val Ala	
145	150
	155
	160

agt tgc gat aag ggg ctt ccg gcc acc atg atg gca ctc gcc gcg cag	528
Ser Cys Asp Lys Gly Leu Pro Ala Thr Met Met Ala Leu Ala Ala Gln	
165	170
	175

cac aac atc gca acc gtg ctg gtc ccc ggc ggc gcg acg ctg ccc gca	576
His Asn Ile Ala Thr Val Leu Val Pro Gly Gly Ala Thr Leu Pro Ala	
180	185
	190

aag gat gga gaa gac aac ggc aag gtgcaa acc att ggc gca cgc ttc	624
Lys Asp Gly Glu Asp Asn Gly Lys Val Gln Thr Ile Gly Ala Arg Phe	
195	200
	205

gcc aat ggc gaa tta tct cta cag gac gca cgc cgt gcg ggc tgt aaa	672
Ala Asn Gly Glu Leu Ser Leu Gln Asp Ala Arg Arg Ala Gly Cys Lys	
210	215
	220

gcc tgt gcc tct tcc ggc ggc ggc tgt caa ttt ttg ggc act gcc ggg	720
Ala Cys Ala Ser Ser Gly Gly Gly Cys Gln Phe Leu Gly Thr Ala Gly	
225	230
	235
	240

aca tct cag gtg gtg gcc gaa gga ttg gga ctg gca atc cca cat tca	768
Thr Ser Gln Val Val Ala Glu Gly Leu Ala Ile Pro His Ser	
245	250
	255

TABLE 4-continued

Coding sequences for *E. coli* yjhG xylonate dehydratase.
SEQ ID NO: 7 and SEQ ID NO: 8

gcc ctg gcc cct tcc ggt gag cct gtg tgg cgg gag atc gcc aga gct	816
Ala Leu Ala Pro Ser Gly Glu Pro Val Trp Arg Glu Ile Ala Arg Ala	
260 265 270	
tcc gcg cga gct gcg ctg aac ctg agt caa aaa ggc atc acc acc cgg	864
Ser Ala Arg Ala Ala Leu Asn Leu Ser Gln Lys Gly Ile Thr Thr Arg	
275 280 285	
gaa att ctc acc gat aaa gcg ata gag aat gcg atg acg gtc cat gcc	912
Glu Ile Leu Thr Asp Lys Ala Ile Glu Asn Ala Met Thr Val His Ala	
290 295 300	
gcg ttc ggt gtc tca aca aac ctg ctg tta cac atc ccg gca att gct	960
Ala Phe Gly Gly Ser Thr Asn Leu Leu His Ile Pro Ala Ile Ala	
305 310 315 320	
cac cag gca ggt tgc cat atc ccg acc gtt gat gac tgg atc cgc atc	1008
His Gln Ala Gly Cys His Ile Pro Thr Val Asp Asp Trp Ile Arg Ile	
325 330 335	
aac aag cgc gtg ccc cga ctg gtg agc gta ctg cct aat ggc ccg gtt	1056
Asn Lys Arg Val Pro Arg Leu Val Ser Val Leu Pro Asn Gly Pro Val	
340 345 350	
tat cat cca acg gtc aat gcc ttt atg gca ggt ggt gtg ccg gaa gtc	1104
Tyr His Pro Thr Val Asn Ala Phe Met Ala Gly Gly Val Pro Glu Val	
355 360 365	
atg ttg cat ctg cgc agc ctc gga ttg ttg cat gaa gac gtt atg acg	1152
Met Leu His Leu Arg Ser Leu Gly Leu Leu His Glu Asp Val Met Thr	
370 375 380	
gtt acc ggc acg acg ctg aaa gaa aac ctc gac tgg tgg gag cac tcc	1200
Val Thr Gly Ser Thr Leu Lys Glu Asn Leu Asp Trp Trp Glu His Ser	
385 390 395 400	
gaa cgg cgt cag cgg ttc aagcaa ctc ctg ctc gat cag gaa caa atc	1248
Glu Arg Arg Gln Arg Phe Lys Gln Leu Leu Asp Gln Glu Gln Ile	
405 410 415	
aac gct gac gaa gtg atc atg tct ccg cag caa gca aaa gcg cgc gga	1296
Asn Ala Asp Glu Val Ile Met Ser Pro Gln Gln Ala Lys Ala Arg Gly	
420 425 430	
tta acc tca act atc acc ttc ccg gtg ggc aat att gcg cca gaa ggt	1344
Leu Thr Ser Thr Ile Thr Phe Pro Val Gly Asn Ile Ala Pro Glu Gly	
435 440 445	
tcg gtg atc aaa tcc acc gcc att gac ccc tcg atg att gat gag caa	1392
Ser Val Ile Lys Ser Thr Ala Ile Asp Pro Ser Met Ile Asp Glu Gln	
450 455 460	
ggt atc tat tac cat aaa ggt gtg gcg aag gtt tat ctg tcc gag aaa	1440
Gly Ile Tyr Tyr His Lys Gly Val Ala Lys Val Tyr Leu Ser Glu Lys	
465 470 475 480	
agt gcg att tac gat atc aaa cat gac aag atc aag gcg ggc gat att	1488
Ser Ala Ile Tyr Asp Ile Lys His Asp Lys Ile Lys Ala Gly Asp Ile	
485 490 495	
ctg gtc att att ggc gtt gga cct tca ggt aca ggg atg gaa gaa acc	1536
Leu Val Ile Ile Gly Val Gly Pro Ser Gly Thr Gly Met Glu Glu Thr	
500 505 510	
tac cag gtt acc agt gcc ctg aag cat ctg tca tac ggt aag cat gtt	1584
Tyr Gln Val Thr Ser Ala Leu Lys His Leu Ser Tyr Gly Lys His Val	
515 520 525	
tcg tta atc acc gat gca cgt ttc tcg ggc gtt tct act ggc gcg tgc	1632
Ser Leu Ile Thr Asp Ala Arg Phe Ser Gly Val Ser Thr Gly Ala Cys	
530 535 540	
atc ggc cat gtg ggg cca gaa gcg ctg gcc gga ggc ccc atc ggt aaa	1680
Ile Gly His Val Gly Pro Glu Ala Leu Ala Gly Gly Pro Ile Gly Lys	
545 550 555 560	
tta cgc acc ggg gat tta att gaa att aaa att gat tgt cgc gag ctt	1728

TABLE 4-continued

Coding sequences for <i>E. coli</i> yjhG xylonate dehydratase.																	
SEQ ID NO: 7 and SEQ ID NO: 8																	
Leu	Arg	Thr	Gly	Asp	Leu	Ile	Glu	Ile	Lys	Ile	Asp	Cys	Arg	Glu	Leu		
565						570										575	
cac	ggc	gaa	gtc	aat	tcc	ctc	gga	acc	cgt	agc	gat	gaa	caa	tta	cct	1776	
His	Gly	Glu	Val	Asn	Phe	Leu	Gly	Thr	Arg	Ser	Asp	Glu	Gln	Leu	Pro		
580							585									590	
tca	cag	gag	gca	act	gca	ata	tta	aat	gcc	aga	ccc	agc	cat	cag		1824	
Ser	Gln	Glu	Glu	Ala	Thr	Ala	Ile	Leu	Asn	Ala	Arg	Pro	Ser	His	Gln		
595							600									605	
gat	tta	ctt	ccc	gat	cct	gaa	ttg	cca	gat	gat	acc	cgg	cta	tgg	gca	1872	
Asp	Leu	Leu	Pro	Asp	Pro	Glu	Leu	Pro	Asp	Asp	Thr	Arg	Leu	Trp	Ala		
610						615										620	
atg	ctt	cag	gcc	gtg	agt	ggt	ggg	aca	tgg	acc	ggt	tgt	att	tat	gat	1920	
Met	Leu	Gln	Ala	Val	Ser	Gly	Gly	Thr	Trp	Thr	Gly	Cys	Ile	Tyr	Asp		
625						630			635							640	
gta	aac	aaa	att	ggc	gcg	gct	ttg	cgc	gat	ttt	atg	aat	aaa	aac	tga	1968	
Val	Asn	Lys	Ile	Gly	Ala	Ala	Leu	Arg	Asp	Phe	Met	Asn	Lys	Asn			
645							650									655	

TABLE 5

Amino acid sequence for <i>Pseudomonas pudita</i> benzoylformate decarboxylase.	
(SEQ ID NO: 9)	
MASVHGTTYELLRRQGIDTVPGNPGSNELPFLKDFPEDFRYLALQEAC	
VVGIAADGYAQASRKPAFINLHSAAGTGNAMGALSNAWNNSHSPLIVTAGQ	
QTRAMIGVEALLTNVDAANLPRPLVKWSYEPASAAEVPHAMSRAIHMAS	
MAPQGPVYLSVPYDDWDKDADPQSHHLFDRHVSSEVRLLNDQDDILVKA	
LNSASNPAPIVLGPDVDAANANADCVMLAERLKAPVWWAPSAPRCPPTR	
HPCFRGLMPAGIAAIASQLLEGHDVVVLVIGAPVFRYHQYDPGQYKLPGTR	

25

TABLE 5-continued

Amino acid sequence for <i>Pseudomonas pudita</i> benzoylformate decarboxylase.	
30	LISVTCDPLEAARAPMGDAIVADIGAMASALANLVEESSRQLPTAAPEP
AKVDQDAGRLLHPETVFDTLNDMAPENAIYLNESTTTAQMWQRNLNMNP	
GSYYFCAGGLGFALPAAIGVQLAEPERQVIAVIGDGSANYSISALWTA	
35	AQYNIPTIFVIMNNGTYGALRWFAVGVLEAENVPGLDVPGIDFRALAKGY
	GVQALKADNLEQLKGSLQEALSAKGPVLIEVSTVSPVK

Other amino acid sequences having benzoylformate decarboxylase activity that can be used in the methods and compositions of the disclosure include:

SEQ ID NO:	ACCESSION NO.	DESCRIPTION
13	ABN80423.1	benzoylformate decarboxylase (<i>Pseudomonas stutzeri</i>)
14	YP_002546713.1	benzoylformate decarboxylase (<i>Agrobacterium radiobacter</i> K84)
15	YP_001350945.1	benzoylformate decarboxylase (<i>Pseudomonas aeruginosa</i> PA7)
16	NP_253588.1	benzoylformate decarboxylase (<i>Pseudomonas aeruginosa</i> PA01)
17	YP_793369.1	benzoylformate decarboxylase (<i>Pseudomonas aeruginosa</i> UCBPP-PA14)
18	ZP_04937527.1	benzoylformate decarboxylase (<i>Pseudomonas aeruginosa</i> 2192)
19	ZP_01367918.1	hypothetical protein PaerPA_01005073 (<i>Pseudomonas aeruginosa</i> PACS2)
20	YP_002442865.1	benzoylformate decarboxylase (<i>Pseudomonas aeruginosa</i> LESB58)
21	CAK95977.1	benzoylformate decarboxylase (<i>Pseudomonas putida</i>)
22	CAK95976.1	benzoylformate decarboxylase (<i>Pseudomonas putida</i>)
23	YP_260581.1	benzoylformate decarboxylase (<i>Pseudomonas fluorescens</i> Pf-5)
24	ZP_06547677.1	benzoylformate decarboxylase (<i>Klebsiella</i> sp. 1_1_55)
25	YP_555151.1	benzoylformate decarboxylase (<i>Burkholderia xenovorans</i> LB400)
26	YP_002363219.1	benzoylformate decarboxylase (<i>Methylocella silvestris</i> BL2)
27	YP_831380.1	benzoylformate decarboxylase (<i>Arthrobacter</i> sp. FB24)
28	YP_572370.1	benzoylformate decarboxylase (<i>Chromohalobacter salexigens</i> DSM 3043)
29	YP_702946.1	benzoylformate decarboxylase (<i>Rhodococcus jostii</i> RHA1)
30	YP_702758.1	benzoylformate decarboxylase (<i>Rhodococcus jostii</i> RHA1)
31	YP_001105345.1	benzoylformate decarboxylase (<i>Saccharopolyspora erythraea</i> NRRL 2338)
32	ZP_06526521.1	benzoylformate decarboxylase (<i>Streptomyces lividans</i> TK24)
33	NP_631486.1	benzoylformate decarboxylase (<i>Streptomyces coelicolor</i> A3(2))
34	ZP_05521701.1	benzoylformate decarboxylase (<i>Streptomyces lividans</i> TK24)
35	CAJ89675.1	putative decarboxylase (<i>Streptomyces ambofaciens</i> ATCC 23877)

-continued

SEQ ID NO:	ACCESSION NO.	DESCRIPTION
36	ZP_04996569.1	benzoylformate decarboxylase (<i>Streptomyces</i> sp. Mg1)
37	ZP_05915352.1	benzoylformate decarboxylase (<i>Brevibacterium linens</i> BL2)
38	YP_885985.1	benzoylformate decarboxylase (<i>Mycobacterium smegmatis</i> str. MC2 155)
39	ZP_05973486.1	benzoylformate decarboxylase (<i>Providencia rustigianii</i> DSM 4541)
40	YP_002754411.1	benzoylformate decarboxylase (<i>Acidobacterium capsulatum</i> ATCC 51196)
41	YP_002954549.1	putative benzoylformate decarboxylase (<i>Desulfovibrio magneticus</i> RS-1)
42	ZP_03572222.1	benzoylformate decarboxylase (bfd) (bfdc) (<i>Burkholderia multivorans</i> CGD2M)
43	ZP_03584382.1	benzoylformate decarboxylase (<i>Burkholderia multivorans</i> CGD1)
44	YP_001578906.1	benzoylformate decarboxylase (<i>Burkholderia multivorans</i> ATCC 17616)
45	YP_001242472.1	benzoylformate decarboxylase (<i>Bradyrhizobium</i> sp. BTA1)
46	NP_773888.1	benzoylformate decarboxylase (<i>Bradyrhizobium japonicum</i> USDA 110)
47	YP_002231898.1	benzoylformate decarboxylase (<i>Burkholderia cenocepacia</i> J2315)
48	ZP_04940696.1	Pyruvate decarboxylase (<i>Burkholderia cenocepacia</i> PC184)
49	YP_836226.1	benzoylformate decarboxylase (<i>Burkholderia cenocepacia</i> HI2424)
50	YP_001765890.1	benzoylformate decarboxylase (<i>Burkholderia cenocepacia</i> MC0-3)
51	NP_773056.1	benzoylformate decarboxylase (<i>Bradyrhizobium japonicum</i> USDA 110)
52	NP_946955.1	benzoylformate decarboxylase (<i>Rhodopseudomonas palustris</i> CGA009)
53	YP_370152.1	benzoylformate decarboxylase (<i>Burkholderia</i> sp. 383)
54	YP_001562574.1	benzoylformate decarboxylase (<i>Delftia acidovorans</i> SPH-1)
55	YP_001203568.1	benzoylformate decarboxylase (<i>Bradyrhizobium</i> sp. ORS278)

TABLE 6

Amino acid sequence of ADHP alcohol dehydrogenase (*E. coli*)
 (SEQ ID NO: 10)
 MQNIIIRKGGMKAAVVTKDHHVDVTYKTLRSLKHGEALLKMECCGVCHT
 DLHVKNNGDFGDKTGVLGHEGIGVVAEVGPVGTVSLKPGDRASVAWFYEG
 CGHCEYCNSGNETLCRSVKNAGYSVDGGMAECCIVVADYAVKVPDGLDS
 AAASSITCAGVTTYKAVKLSKIRPGQWIAIYGLGGLGNLALQYAKNVFN
 AKVIAIDVNDEQLKLATEMGADLAINSHTEDAAKIVQEKTGGAHAAVV

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TABLE 6 - continued

Amino acid sequence of ADHP alcohol dehydrogenase (*E. coli*)
 (SEQ ID NO: 10)
 AVAKAAFNSAVDAVRAGGRVVAVGLPPESMSLDIPRLVLDGIEVVVGSLV
 GTRQDLTEAFQFAAEKGVVPKVALRPLADINTIFTEMEEGKIRGRMVID
 FRH

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Other sequence having alcohol dehydrogenase activity that may be used in the methods and compositions of the disclosure include, but are not limited to:

SEQ ID NO: ACCESSION NO. DESCRIPTION

56	YP_002292842.1	alcohol dehydrogenase (<i>Escherichia coli</i> SE11)
57	BAB35505.1	alcohol dehydrogenase (<i>Escherichia coli</i> O157:H7 str. <i>Sakai</i>)
58	ACI83654.1	alcohol dehydrogenase (<i>Escherichia coli</i> , str. TB182A)
59	YP_540705.1	alcohol dehydrogenase (<i>Escherichia coli</i> UT189)
60	ABB61735.1	alcohol dehydrogenase (<i>Shigella dysenteriae</i> Sd197)
61	AP_002101.1	alcohol dehydrogenase, 1-propanol preferring (<i>Escherichia coli</i> str. K-12 substr. W3110)
62	YP_001462749.1	alcohol dehydrogenase (<i>Escherichia coli</i> E24377A)
63	NP_310109.2	alcohol dehydrogenase (<i>Escherichia coli</i> O157:H7 str. <i>Sakai</i>)
64	YP_002382641.1	alcohol dehydrogenase (<i>Escherichia fergusonii</i> ATCC 35469)
65	NP_753808.2	alcohol dehydrogenase (<i>Escherichia coli</i> CFT073)
66	ZP_06653399.1	alcohol dehydrogenase (<i>Escherichia coli</i> B354)
67	NP_707612.1	alcohol dehydrogenase (<i>Shigella flexneri</i> 2a str. 301)
68	YP_002329135.1	alcohol dehydrogenase (<i>Escherichia coli</i> O127:H6 str. E2348/69)
69	BAI54933.1	alcohol dehydrogenase (<i>Escherichia coli</i> SE15)
70	YP_669388.1	alcohol dehydrogenase (<i>Escherichia coli</i> 536)
71	YP_403226.2	alcohol dehydrogenase (<i>Shigella dysenteriae</i> Sd197)
72	NP_455923.1	alcohol dehydrogenase (<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhi</i> str. CT18)
73	YP_001587957.1	alcohol dehydrogenase (<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Paratyphi B</i> str. SPB7)
74	YP_002040815.1	alcohol dehydrogenase (<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Newport</i> str. SL254)
75	YP_150561.1	alcohol dehydrogenase (<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Paratyphi A</i> str. ATCC 9150)

SEQ ID NO: ACCESSION NO. DESCRIPTION

76	ZP_03359218.1	alcohol dehydrogenase (<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhi</i> str. E02-1180)
77	YP_002637737.1	alcohol dehydrogenase (<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Paratyphi C</i> strain RKS4594)
78	ZP_05967726.2	alcohol dehydrogenase, propanol-preferring (<i>Enterobacter cancerogenus</i> ATCC 35316)

The term diol dehydratase refers to a polypeptide (or polypeptides) having an enzyme activity that catalyzes the conversion of 1,2,4-D-butanetriol to 4-hydroxy-D-butanal. Diol dehydratase may utilize the cofactor adenosyl cobalamin. For example, a diol dehydratase useful in the methods and compositions of the disclosure can be selected from 2,3-butanediol dehydratase, 3,4-hexanediol dehydratase, 4,5-octanediol dehydratase, 5,6-decanediol dehydratase, 6,7-dodecanediol dehydratase, 7,8-tetradecanediol dehydratase, 8,9-hexadecanediol dehydratase, 2,5-dimethyl-3,4-hexanediol dehydratase, 3,6-dimethyl-4,5-octanediol dehydratase, 2,7-dimethyl-4,5-octanediol dehydratase, 2,9-dimethyl-5,6-decanediol dehydratase, 1,4-diphenyl-2,3-butanediol dehydratase, bis-1,4-(4-hydroxyphenyl)-2,3-butanediol dehydratase, 1,4-diindole-2,3-butanediol dehydratase, 1,2-cyclopentanediol dehydratase, 2,3-pantanediol dehydratase, 2,3-hexanediol dehydratase, 2,3-heptanediol dehydratase, 2,3-octanediol dehydratase, 2,3-nonenediol dehydratase, 4-methyl-2,3-pantanediol dehydratase, 4-methyl-2,3-hexanediol dehydratase, 5-methyl-2,3-hexanediol dehydratase, 6-methyl-2,3-heptanediol dehydratase, 1-phenyl-2,3-butanediol dehydratase, 1-(4-hydroxyphenyl)-2,3-butanediol dehydratase, 1-indole-2,3-butanediol dehydratase, 3,4-heptanediol dehydratase, 3,4-octanediol dehydratase, 3,4-nonenediol dehydratase, 3,4-decanediol dehydratase, 3,4-undecanediol dehydratase, 2-methyl-3,4-hexanediol dehydratase, 5-methyl-3,4-heptanediol dehydratase, 6-methyl-3,4-heptanediol dehydratase, 7-methyl-3,4-octanediol dehydratase, 1-phenyl-2,3-pantanediol dehydratase, 1-(4-hydroxyphenyl)-2,3-pantanediol dehydratase, 1-indole-2,3-pantanediol dehydratase, 4,5-nonanediol dehydratase, 4,5-decanediol dehydratase, 4,5-undecanediol dehydratase, 4,5-dodecanediol dehydratase, 2-methyl-3,4-heptanediol dehydratase, 3-methyl-4,5-octanediol dehydratase, 2-methyl-4,5-octanediol dehydratase, 8-methyl-4,5-nonanediol dehydratase, 1-phenyl-2,3-hexanediol dehydratase, 1-(4-hydroxyphenyl)-2,3-hexanediol dehydratase, 1-indole-2,3-hexanediol dehydratase, 5,6-undecanediol dehydratase, 5,6-tridecanediol dehydratase, 2-methyl-3,4-octanediol dehydratase, 3-methyl-4,5-nonanediol dehydratase, 2-methyl-4,5-nonanediol dehydratase, 2-methyl-5,6-decanediol dehydratase, 1-phenyl-2,3-heptanediol dehydratase, 1-(4-hydroxyphenyl)-2,3-heptanediol dehydratase, 1-indole-2,3-heptanediol dehydratase, 6,7-tridecanediol dehydratase, 6,7-tetradecanediol dehydratase, 2-methyl-3,4-nonanediol dehydratase, 3-methyl-4,5-decanediol dehydratase, 2-methyl-4,5-decanediol dehydratase, 2-methyl-5,6-undecanediol dehydratase, 1-phenyl-2,3-octanediol dehydratase, 1-(4-hydroxyphenyl)-2,3-octanediol dehydratase, 1-indole-2,3-octanediol dehydratase, 7,8-pentadecanediol dehydratase, 2-methyl-3,4-decanediol dehydratase, 3-methyl-4,5-undecanediol dehydratase, 2-methyl-4,5-undecanediol dehydratase, 2-methyl-5,6-dodecanediol dehydratase, 1-phenyl-2,3-nonenediol dehydratase, 1-(4-hydroxyphenyl)-2,3-nonenediol dehydratase, 1-indole-2,3-nonenediol dehydratase,

dehydratase, 2-methyl-3,4-undecanediol dehydratase, 3-methyl-4,5-dodecanediol dehydratase, 2-methyl-4,5-dodecanediol dehydratase, 2-methyl-5,6-tridecanediol dehydratase, 1-phenyl-2,3-decanediol dehydratase, 1-(4-hydroxyphenyl)-2,3-decanediol dehydratase, 1-indole-2,3-decanediol dehydratase, 2,5-dimethyl-3,4-heptanediol dehydratase, 2,6-dimethyl-3,4-heptanediol dehydratase, 2,7-dimethyl-3,4-octanediol dehydratase, 1-phenyl-4-methyl-2,3-pantanediol dehydratase, 1-(4-hydroxyphenyl)-4-methyl-2,3-pantanediol dehydratase, 1-indole-4-methyl-2,3-pantanediol dehydratase, 2,6-dimethyl-4,5-octanediol dehydratase, 3,8-dimethyl-4,5-nonanediol dehydratase, 1-phenyl-4-methyl-2,3-hexanediol dehydratase, 1-(4-hydroxyphenyl)-4-methyl-2,3-hexanediol dehydratase, 1-indole-4-methyl-2,3-hexanediol dehydratase, 2,8-dimethyl-4,5-nonanediol dehydratase, 1-phenyl-5-methyl-2,3-hexanediol dehydratase, 1-(4-hydroxyphenyl)-5-methyl-2,3-hexanediol dehydratase, 1-indole-5-methyl-2,3-hexanediol dehydratase, 1-phenyl-6-methyl-2,3-heptanediol dehydratase, 1-(4-hydroxyphenyl)-6-methyl-2,3-heptanediol dehydratase, 1-indole-6-methyl-2,3-heptanediol dehydratase, 1-(4-hydroxyphenyl)-4-phenyl-2,3-butanediol dehydratase, 1-indole-4-phenyl-2,3-butanediol dehydratase, 1-indole-4-(4-hydroxyphenyl)-2,3-butanediol dehydratase, 1,10-diamino-5,6-decanediol dehydratase, 1,4-di(4-hydroxyphenyl)-2,3-butanediol, and 2,3-hexanediol-1,6-dicarboxylic acid dehydratase. The diol dehydratase can be one characterized, for example from *Listeria*, *Amycolatopsis*, *Klebsiella*, *Pseudomonas*, *Salmonella*, *Lactobacillus*, *Yersinia*, and the like.

An “alcohol dehydrogenase” refers to any alcohol dehydrogenase enzyme having a catalytic activity that converts 3,4-dihydroxy-D-butanal to D-1,2,4-butanetriol, e.g., an AdhP, or an AdhE or a YiaY type of alcohol dehydrogenase. An alcohol dehydrogenase also refers to an enzyme having a catalytic activity that converts 4-hydroxy-D-butanal to 1,4-butanediol.

Microorganisms provided herein are modified to produce metabolites in quantities not available in the parental microorganism. A “metabolite” refers to any substance produced by metabolism or a substance necessary for, or taking part in, a particular metabolic process. A metabolite can be an organic compound that is a starting material (e.g., D-xylonic acid), an intermediate (e.g., 3,4-dihydroxy-D-butanal), or an end product (e.g., 1,4-butanediol) of metabolism. Metabolites can be used to construct more complex molecules, or they can be broken down into simpler ones. Intermediate metabolites can be synthesized from other metabolites, for example, to be used to make more complex substances, or broken down into simpler compounds, often with the release of chemical energy.

Exemplary metabolites include D-xylose, D-xylonic acid, 3-deoxy-D-glycero-pentulose, 3,4-dihydroxy-D-butanal, 1,2,4-D-butanetriol, 4-hydroxy-D-butanal, and 1,4-butanediol. For example, as shown in FIG. 1, a recombinant microorganism can be metabolically engineered to provide

elevated expression or heterologous expression of enzymes useful in the production of 1,4-butanediol. For example, xylose is converted to xylonic acid by a xylose dehydrogenase. 3-Deoxy-D-glycero-pentulsonic acid is produced by xylonate dehydratase from xylonic acid. 3-Deoxy-D-glycero-pentulsonic acid is further converted by a decarboxylase to 3,4-dihydroxy-D-butanal. 3,4-Dihydroxy-D-butanal is then reduced to 1,2,4-D-butanetriol by a dehydrogenase. 1,2,4-D-butanetriol is further dehydrated into 4-hydroxy-D-butanal by a dehydratase. 4-hydroxy-D-butanal was then reduced to 1,4-butanediol by a dehydrogenase.

In addition, it can be advantageous to decrease or remove expression of enzymes that compete with a metabolite used in the production of 1,4-butanediol. For example, the enzyme D-xylose isomerase (*XylA*) can be reduced or knocked out to prevent flux of the substrate xylose to D-xylulose by the activity of the D-xylose isomerase. Alternatively, or in addition, the enzyme 2-keto acid aldolase (*YagE* and *YjhH*) can be reduced or knocked out to prevent flux of the metabolite 3-deoxy-D-glycero-pentulsonic acid to pyruvic acid. Alternatively, or in addition, the enzyme 2-keto acid transaminase can be reduced or knocked out to prevent flux of the metabolite 3-deoxy-D-glycero-pentulsonic acid to 2-amino-2,3-dideoxy-L-pentanoic acid. Alternatively, or in addition, the enzyme 2-keto acid dehydrogenase may be reduced or knocked out to prevent flux of the metabolite 3-deoxy-D-glycero-pentulsonic acid to 3-deoxy-D-glycero-pentanoic acid.

The disclosure identifies specific genes and enzymes useful in the methods, compositions, and organisms for the production of 1,4-butanediol, or intermediates thereof; however it will be recognized that absolute identity to such genes or polypeptides is not necessary. For example, changes in a particular gene or polynucleotide comprising a sequence encoding a polypeptide or enzyme can be performed and screened for activity. Typically such changes comprise conservative mutations and/or silent mutations. Such modified or mutated polynucleotides and polypeptides can be screened for expression of a functional enzyme activity using methods known in the art.

Due to the inherent degeneracy of the genetic code, other polynucleotides which encode substantially the same or a functionally equivalent polypeptide can also be used to clone and express the polynucleotides encoding such enzymes.

As will be understood by those of skill in the art, it can be advantageous to modify a coding sequence to enhance its expression in a particular host. The genetic code is redundant with 64 possible codons, but most organisms typically use a subset of these codons. The codons that are utilized most often in a species are called optimal codons, and those not utilized very often are classified as rare or low-usage codons. Codons can be substituted to reflect the preferred codon usage of the host, a process sometimes called "codon optimization" or "controlling for species codon bias."

Optimized coding sequences containing codons preferred by a particular prokaryotic or eukaryotic host (see also, Murray et al. (1989) *Nucl. Acids Res.* 17:477-508) can be prepared, for example, to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced from a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, typical stop codons for *S. cerevisiae* and mammals are UAA and UGA, respectively. The typical stop codon for monocotyledonous plants is UGA, whereas insects and *E. coli* commonly use UAA as the stop codon (Dalphin et al. (1996) *Nucl. Acids Res.* 24:216-218). Methodology for opti-

mizing a nucleotide sequence for expression in a plant is provided, for example, in U.S. Pat. No. 6,015,891, and the references cited therein.

Those of skill in the art will recognize that, due to the degenerate nature of the genetic code, a variety of DNA compounds differing in their nucleotide sequences can be used to encode a given amino acid sequence (e.g., enzyme) of the disclosure. The native DNA sequence encoding the biosynthetic enzymes described above are referenced herein merely to illustrate an embodiment of the disclosure, and the disclosure includes DNA compounds of any sequence that encode the amino acid sequences of the polypeptides and proteins of the enzymes utilized in the methods of the disclosure. In similar fashion, a polypeptide can typically tolerate one or more amino acid substitutions, deletions, and insertions in its amino acid sequence without loss or significant loss of a desired activity. The disclosure includes such polypeptides with different amino acid sequences than the specific proteins described herein so long as the modified or variant polypeptides have the enzymatic anabolic or catabolic activity of the reference polypeptide. Furthermore, the amino acid sequences encoded by the DNA sequences shown herein merely illustrate embodiments of the disclosure.

In addition, homologs of enzymes useful for generating metabolites are encompassed by the microorganisms and methods provided herein. The term "homologs" used with respect to an original enzyme or gene of a first family or species refers to distinct enzymes or genes of a second family or species which are determined by functional, structural, or genomic analyses to be an enzyme or gene of the second family or species which corresponds to the original enzyme or gene of the first family or species. Most often, homologs will have functional, structural, or genomic similarities. Techniques are known by which homologs of an enzyme or gene can readily be cloned using genetic probes and PCR. Identity of cloned sequences as homolog can be confirmed using functional assays and/or by genomic mapping of the genes.

A protein has "homology" or is "homologous" to a second protein if the nucleic acid sequence that encodes the protein has a similar sequence to the nucleic acid sequence that encodes the second protein. Alternatively, a protein has homology to a second protein if the two proteins have "similar" amino acid sequences. (Thus, the term "homologous proteins" is defined to mean that the two proteins have similar amino acid sequences).

As used herein, two proteins (or a region of the proteins) are substantially homologous when the amino acid sequences have at least about 30%, 40%, 50% 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity. To determine the percent identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In one embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, typically at least 40%, more typically at least 50%, even more typically at least 60%, and even more typically at least 70%, 80%, 90%, 100% of the length of the reference sequence. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or

nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

When "homologous" is used in reference to proteins or peptides, it is recognized that residue positions that are not identical often differ by conservative amino acid substitutions. A "conservative amino acid substitution" is one in which an amino acid residue is substituted by another amino acid residue having a side chain (R group) with similar chemical properties (e.g., charge or hydrophobicity). In general, a conservative amino acid substitution will not substantially change the functional properties of a protein. In cases where two or more amino acid sequences differ from each other by conservative substitutions, the percent sequence identity or degree of homology may be adjusted upwards to correct for the conservative nature of the substitution. Means for making this adjustment are well known to those of skill in the art. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). In addition, the following five groups each contain amino acids that are conservative substitutions for one another: 1) Serine (S), Threonine (T); 2) Asparagine (N), Glutamine (Q); 3) Arginine (R), Lysine (K); 4) Isoleucine (I), Leucine (L), Methionine (M), Alanine (A), Valine (V), and 5) Phenylalanine (F), Tyrosine (Y), Tryptophan (W).

Sequence homology for polypeptides, which is also referred to as percent sequence identity, is typically measured using sequence analysis software. See, e.g., the Sequence Analysis Software Package of the Genetics Computer Group (GCG), University of Wisconsin Biotechnology Center, 910 University Avenue, Madison, Wis. 53705. Protein analysis software matches similar sequences using measure of homology assigned to various substitutions, deletions, and other modifications, including conservative amino acid substitutions. For instance, GCG contains programs such as "Gap" and "Bestfit" which can be used with default parameters to determine sequence homology or sequence identity between closely related polypeptides, such as homologous polypeptides from different species of organisms or between a wild type protein and a mutein thereof. See, e.g., GCG Version 6.1.

A typical algorithm used comparing a molecule sequence to a database containing a large number of sequences from different organisms is the computer program BLAST, as is known in the art, especially blastp or tblastn. Typical parameters for BLASTp are: Expectation value: 10 (default); Filter: seg (default); Cost to open a gap: 11 (default); Cost to extend a gap: 1 (default); Max. alignments: 100 (default); Word size: 11 (default); No. of descriptions: 100 (default); Penalty Matrix: BLOWSUM62.

When searching a database containing sequences from a large number of different organisms, it is typical to compare amino acid sequences. Database searching using amino acid sequences can be measured by algorithms other than blastp known in the art. For instance, polypeptide sequences can be compared using FASTA, a program in GCG Version 6.1. FASTA provides alignments and percent sequence identity of the regions of the best overlap between the query and search

sequences. For example, percent sequence identity between amino acid sequences can be determined using FASTA with its default parameters (a word size of 2 and the PAM250 scoring matrix), as provided in GCG Version 6.1, hereby incorporated herein by reference.

The disclosure provides accession numbers for various genes and/or proteins, homologs, and variants useful in the generation of recombinant microorganism described herein. In addition, the nucleotide and amino acid sequences corresponding to the accession numbers are provided in the attached Sequence Listing. It is to be understood that homologs and variants described herein are exemplary and non-limiting. Additional homologs, variants, and polynucleotide and/or amino acid sequences are available to those of skill in the art using various databases including, for example, the National Center for Biotechnology Information (NCBI) access to which is available on the World-Wide-Web.

It is understood that a range of microorganisms can be modified to include a recombinant metabolic pathway suitable for the production of 1,4-butanediol. It is also understood that various microorganisms can act as "sources" for genetic material encoding target enzymes suitable for use in a recombinant microorganism provided herein. The term "microorganism" includes prokaryotic and eukaryotic microbial species from the Domains Archaea, Bacteria, and Eucarya, the latter including yeast and filamentous fungi, protozoa, algae, or higher Protista. The terms "microbial cells" and "microbes" are used interchangeably with the term microorganism.

The term "prokaryotes" is art recognized and refers to cells which contain no nucleus or other cell organelles. The prokaryotes are generally classified in one of two domains, the Bacteria and the Archaea. The definitive difference between organisms of the Archaea and Bacteria domains is based on fundamental differences in the nucleotide base sequence in the 16S ribosomal RNA.

The term "Archaea" refers to a categorization of organisms of the division Membosicutes, typically found in unusual environments and distinguished from the rest of the prokaryotes by several criteria, including the number of ribosomal proteins and the lack of muramic acid in cell walls. On the basis of ssrRNA analysis, the Archaea consist of two phylogenetically-distinct groups: Crenarchaeota and Euryarchaeota. On the basis of their physiology, the Archaea can be organized into three types: methanogens (prokaryotes that produce methane); extreme halophiles (prokaryotes that live at very high concentrations of salt ((NaCl)); and extreme (hyper) thermophilus (prokaryotes that live at very high temperatures). Besides the unifying archaeal features that distinguish them from Bacteria (i.e., no murein in cell wall, ester-linked membrane lipids, and the like), these prokaryotes exhibit unique structural or biochemical attributes which adapt them to their particular habitats. The Crenarchaeota consists mainly of hyperthermophilic sulfur-dependent prokaryotes and the Euryarchaeota contains the methanogens and extreme halophiles.

"Bacteria", or "eubacteria", refers to a domain of prokaryotic organisms. Bacteria include at least 11 distinct groups as follows: (1) Gram-positive (gram+) bacteria, of which there are two major subdivisions: (1) high G+C group (*Actinomycetes*, *Mycobacteria*, *Micrococcus*, others) (2) low G+C group (*Bacillus*, *Clostridia*, *Lactobacillus*, *Staphylococci*, *Streptococci*, *Mycoplasmas*); (2) Proteobacteria, e.g., Purple photosynthetic+non-photosynthetic Gram-negative bacteria (includes most "common" Gram-negative bacteria); (3) Cyanobacteria, e.g., oxygenic phototrophs; (4) Spirochetes and related species; (5) Planctomyces; (6) *Bacteroides*, *Fla-*

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vobacteria; (7) *Chlamydia*; (8) Green sulfur bacteria; (9) Green non-sulfur bacteria (also anaerobic phototrophs); (10) Radioresistant micrococci and relatives; and (11) Thermo-toga and Thermosiphon thermophiles.

"Gram-negative bacteria" include cocci, nonenteric rods, and enteric rods. The genera of Gram-negative bacteria include, for example, *Neisseria*, *Spirillum*, *Pasteurella*, *Bacillus*, *Yersinia*, *Francisella*, *Haemophilus*, *Bordetella*, *Escherichia*, *Salmonella*, *Shigella*, *Klebsiella*, *Proteus*, *Vibrio*, *Pseudomonas*, *Bacteroides*, *Acetobacter*, *Aerobacter*, *Agrobacterium*, *Azotobacter*, *Spirilla*, *Serratia*, *Vibrio*, *Rhizobium*, *Chlamydia*, *Rickettsia*, *Treponema*, and *Fusobacterium*.

"Gram positive bacteria" include cocci, nonsporulating rods, and sporulating rods. The genera of gram positive bacteria include, for example, *Actinomyces*, *Bacillus*, *Clostridium*, *Corynebacterium*, *Erysipelothrix*, *Lactobacillus*, *Listeria*, *Mycobacterium*, *Myxococcus*, *Nocardia*, *Staphylococcus*, *Streptococcus*, and *Streptomyces*.

The term "recombinant microorganism" and "recombinant host cell" are used interchangeably herein and refer to microorganisms that have been genetically modified to express or over-express endogenous polynucleotides, or to express non-endogenous polynucleotides, such as those included in a vector, or which have a reduction in expression of an endogenous gene. The polynucleotide generally encodes a target enzyme involved in a metabolic pathway for producing a desired metabolite as described above. Accordingly, recombinant microorganisms described herein have been genetically engineered to express or over-express target enzymes not previously expressed or over-expressed by a parental microorganism. It is understood that the terms "recombinant microorganism" and "recombinant host cell" refer not only to the particular recombinant microorganism but to the progeny or potential progeny of such a microorganism.

A "parental microorganism" refers to a cell used to generate a recombinant microorganism. The term "parental microorganism" describes a cell that occurs in nature, i.e., a "wild-type" cell that has not been genetically modified. The term "parental microorganism" also describes a cell that has been genetically modified but which does not express or over-express a target enzyme, e.g., an enzyme involved in the biosynthetic pathway for the production of a desired metabolite. For example, a wild-type microorganism can be genetically modified to express or over-express a first target enzyme such as a xylose dehydrogenase. This microorganism can act as a parental microorganism in the generation of a microorganism modified to express or over-express a second target enzyme, e.g., xylonate dehydratase. In turn, the microorganism modified to express or over-express, e.g., a xylose dehydrogenase and a xylonate dehydratase can be modified to express or over-express a third target enzyme, e.g., a benzoylformate decarboxylase. Accordingly, a parental microorganism functions as a reference cell for successive genetic modification events. Each modification event can be accomplished by introducing a nucleic acid molecule into the reference cell. The introduction facilitates the expression or over-expression of a target enzyme. It is understood that the term "facilitates" encompasses the activation of endogenous polynucleotides encoding a target enzyme through genetic modification of, e.g., a promoter sequence in a parental microorganism. It is further understood that the term "facilitates" encompasses the introduction of exogenous polynucleotides encoding a target enzyme into a parental microorganism.

In another embodiment a method of producing a recombinant microorganism that converts a suitable carbon substrate to 1,4-butanediol is provided. The method includes trans-

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forming a microorganism with one or more recombinant polynucleotides encoding polypeptides that include, for example, D-xylonate dehydrogenase, D-xylonate dehydratase, benzoylformate decarboxylase, diol dehydratase, and an alcohol dehydrogenase. Polynucleotides that encode enzymes useful for generating metabolites including homologs, variants, fragments, related fusion proteins, or functional equivalents thereof, are used in recombinant nucleic acid molecules that direct the expression of such polypeptides in appropriate host cells, such as bacterial or yeast cells. It is understood that the addition of sequences which do not alter the encoded activity of a polynucleotide, such as the addition of a non-functional or non-coding sequence, is a conservative variation of the basic nucleic acid. The "activity" of an enzyme is a measure of its ability to catalyze a reaction resulting in a metabolite, i.e., to "function", and may be expressed as the rate at which the metabolite of the reaction is produced. For example, enzyme activity can be represented as the amount of metabolite produced per unit of time or per unit of enzyme (e.g., concentration or weight), or in terms of affinity or dissociation constants.

A "protein" or "polypeptide", which terms are used interchangeably herein, comprises one or more chains of chemical building blocks called amino acids that are linked together by chemical bonds called peptide bonds. An "enzyme" means any substance, composed wholly or largely of protein, that catalyzes or promotes, more or less specifically, one or more chemical or biochemical reactions. A "native" or "wild-type" protein, enzyme, polynucleotide, gene, or cell, means a protein, enzyme, polynucleotide, gene, or cell that occurs in nature.

It is understood that the polynucleotides described above include "genes" and that the nucleic acid molecules described above include "vectors" or "plasmids." Accordingly, the term "gene", also called a "structural gene" refers to a polynucleotide that codes for a particular sequence of amino acids, which comprise all or part of one or more proteins or enzymes, and can include regulatory (non-transcribed) DNA sequences, such as promoter sequences, which determine, for example, the conditions under which the gene is expressed. The transcribed region of the gene can include untranslated regions, including introns, 5'-untranslated region (UTR), and 3'-UTR, as well as the coding sequence. The term "nucleic acid" or "recombinant nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term "expression" with respect to a gene sequence refers to transcription of the gene and, as appropriate, translation of the resulting mRNA transcript to a protein. Thus, as will be clear from the context, expression of a protein results from transcription and translation of an open reading frame sequence.

The term "operon" refers to two or more genes which are transcribed as a single transcriptional unit from a common promoter. In some embodiments, the genes comprising the operon are contiguous genes. It is understood that transcription of an entire operon can be modified (i.e., increased, decreased, or eliminated) by modifying the common promoter. Alternatively, any gene or combination of genes in an operon can be modified to alter the function or activity of the encoded polypeptide. The modification can result in an increase in the activity of the encoded polypeptide. Further, the modification can impart new activities on the encoded polypeptide. Exemplary new activities include the use of alternative substrates and/or the ability to function in alternative environmental conditions.

A "vector" is any means by which a nucleic acid can be propagated and/or transferred between organisms, cells, or

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cellular components. Vectors can include viruses, bacteriophages, pro-viruses, plasmids, phagemids, transposons, and artificial chromosomes, such as YACs (yeast artificial chromosomes), BACs (bacterial artificial chromosomes), PLACs (plant artificial chromosomes), and the like, that are "episomes," that is, that replicate autonomously or can integrate into a chromosome of a host cell. A vector can also be a naked RNA polynucleotide, a naked DNA polynucleotide, a polynucleotide composed of both DNA and RNA within the same strand, a poly-lysine-conjugated DNA or RNA, a peptide-conjugated DNA or RNA, a liposome-conjugated DNA, or the like, that are not episomal in nature, or it can be an organism which comprises one or more of the above polynucleotide constructs such as an *agrobacterium* or a bacterium.

"Transformation" refers to the process by which a vector is introduced into a host cell. Transformation (or transduction, or transfection), can be achieved by any one of a number of means including electroporation, microinjection, biolistics (or particle bombardment-mediated delivery), or *agrobacterium* mediated transformation.

The disclosure provides nucleic acid molecules in the form of recombinant DNA expression vectors or plasmids, as described in more detail below, that encode one or more target enzymes. Generally, such vectors can either replicate in the cytoplasm of the host microorganism or integrate into the chromosomal DNA of the host microorganism. In either case, the vector can be a stable vector (i.e., the vector remains present over many cell divisions, even if only with selective pressure) or a transient vector (i.e., the vector is gradually lost by host microorganisms with increasing numbers of cell divisions). The disclosure provides DNA molecules in isolated (i.e., not pure, but existing in a preparation in an abundance and/or concentration not found in nature) and purified (i.e., substantially free of contaminating materials or substantially free of materials with which the corresponding DNA would be found in nature) forms.

Provided herein are methods for the heterologous expression of one or more of the biosynthetic genes involved in 1,4-butanediol biosynthesis and recombinant DNA expression vectors useful in the method. Thus, included within the scope of the disclosure are recombinant expression vectors that include such nucleic acids. The term "expression vector" refers to a nucleic acid that can be introduced into a host microorganism or cell-free transcription and translation system. An expression vector can be maintained permanently or transiently in a microorganism, whether as part of the chromosomal or other DNA in the microorganism or in any cellular compartment, such as a replicating vector in the cytoplasm. An expression vector also comprises a promoter that drives expression of an RNA, which typically is translated into a polypeptide in the microorganism or cell extract. For efficient translation of RNA into protein, the expression vector also typically contains a ribosome-binding site sequence positioned upstream of the start codon of the coding sequence of the gene to be expressed. Other elements, such as enhancers, secretion signal sequences, transcription termination sequences, and one or more marker genes by which host microorganisms containing the vector can be identified and/or selected, may also be present in an expression vector. Selectable markers, i.e., genes that confer antibiotic resistance or sensitivity, are used and confer a selectable phenotype on transformed cells when the cells are grown in an appropriate selective medium.

The various components of an expression vector can vary widely, depending on the intended use of the vector and the host cell(s) in which the vector is intended to replicate or drive

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expression. Expression vector components suitable for the expression of genes and maintenance of vectors in *E. coli*, yeast, *Streptomyces*, and other commonly used cells are widely known and commercially available. For example, suitable promoters for inclusion in the expression vectors of the disclosure include those that function in eukaryotic or prokaryotic host microorganisms. Promoters can comprise regulatory sequences that allow for regulation of expression relative to the growth of the host microorganism or that cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus. For *E. coli* and certain other bacterial host cells, promoters derived from genes for biosynthetic enzymes, antibiotic-resistance conferring enzymes, and phage proteins can be used and include, for example, the galactose, lactose (*lac*), maltose, tryptophan (*trp*), beta-lactamase (*bla*), bacteriophage lambda PL, and T5 promoters. In addition, synthetic promoters, such as the tac promoter (U.S. Pat. No. 4,551,433), can also be used. For *E. coli* expression vectors, it is useful to include an *E. coli* origin of replication, such as from pUC, p1P, p1, pBR, and the like.

Thus, recombinant expression vectors contain at least one expression system, which, in turn, is composed of at least a portion of polyketide synthase (PKS) and/or other biosynthetic gene coding sequences operably linked to a promoter and optionally termination sequences that operate to effect expression of the coding sequence in compatible host cells. The host cells are modified by transformation with the recombinant DNA expression vectors of the disclosure to contain the expression system sequences either as extrachromosomal elements or integrated into the chromosome.

A nucleic acid of the disclosure can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques as known in the art. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to nucleotide sequences can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

It is also understood that an isolated nucleic acid molecule encoding a polypeptide homologous to the enzymes described herein can be created by introducing one or more nucleotide substitutions, additions, or deletions into the nucleotide sequence encoding the particular polypeptide, such that one or more amino acid substitutions, additions, or deletions are introduced into the encoded protein. Mutations can be introduced into the polynucleotide by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. In contrast to those positions where it may be desirable to make a non-conservative amino acid substitution (see above), in some positions it is preferable to make conservative amino acid substitutions.

In another embodiment a method for producing 1,4-butanediol is provided. The method includes culturing a recombinant microorganism as provided herein in the presence of a suitable substrate and under conditions suitable for the conversion of the substrate to 1,4-butanediol or an intermediate which can be further converted to 1,4-butanediol. The 1,4-butanediol produced by a microorganism provided herein can be detected by any method known to the skilled artisan. Such methods include mass spectrometry. Culture conditions suitable for the growth and maintenance can be modified to accommodate the requirements of each microorganism.

As previously discussed, general texts which describe molecular biological techniques useful herein, including the use of vectors, promoters and many other relevant topics, include Berger and Kimmel, Guide to Molecular Cloning

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Techniques, Methods in Enzymology Volume 152, (Academic Press, Inc., San Diego, Calif.) ("Berger"); Sambrook et al., Molecular Cloning: A Laboratory Manual, 2d ed., Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1989 ("Sambrook"); and Current Protocols in Molecular Biology, F. M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 1999) ("Ausubel"). Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR), the ligase chain reaction (LCR), Q β -replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the disclosure are found in Berger, Sambrook, and Ausubel, as well as in Mullis et al. (1987) U.S. Pat. No. 4,683,202; Innis et al., eds. (1990) PCR Protocols: A Guide to Methods and Applications (Academic Press Inc. San Diego, Calif.) ("Innis"); Arnheim & Levinson (Oct. 1, 1990) *C&EN* 36:47; Kwok et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:1173; Guatelli et al. (1990) *Proc. Nat'l Acad. Sci. USA* 87:1874; Lomell et al. (1989) *J. Clin. Chem.* 35:1826; Landegren et al. (1988) *Science* 241: 1077-1080; Van Brunt (1990) *Biotechnology* 8:291-294; Wu and Wallace (1989) *Gene* 4:560; Barringer et al. (1990) *Gene* 89:117; and Sooknanan and Malek (1995) *Biotechnology* 13:563-564. Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) *Nature* 369:684-685 and the references cited therein, in which PCR amplicons of up to 40 kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion, and sequencing using reverse transcriptase and a polymerase. See, e.g., Ausubel, Sambrook and Berger, all supra.

Appropriate culture conditions are conditions of culture medium pH, ionic strength, nutritive content, and the like; temperature; oxygen/CO₂/nitrogen content; humidity; and other culture conditions that permit production of the compound by the host microorganism, i.e., by the metabolic action of the microorganism. Appropriate culture conditions are well known to the skilled artisan for the various microorganisms that can serve as host cells.

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EXAMPLES

Escherichia coli strain JCL16 (BW25113/F' [traD36, proAB+, lacIqZΔM15Tn10]) was successfully modified to produce 1,4-butanediol from D-xylonic acid using the pathway illustrated in FIG. 2.

In addition to the genes already expressed by *E. coli* (e.g., yagF, yjhG, and yqhD), the benzoylformate decarboxylase of *Pseudomonas putida* (mdlC) and the diol dehydratases from *Klebsiella pneumoniae* (gldABC), *Klebsiella oxytoca* (pddABC), or *Clostridium butyricum* (dhaB123) were expressed heterologously behind the PLLacO1 inducible promoter (FIG. 3).

Diol dehydratases do not naturally utilize 1,2,4-butanetriol as a substrate. To illustrate that the diol dehydratases are able to utilize 1,2,4-butanetriol, diol dehydratase activity was determined. All of the diol dehydratases examined, GldABC, PddABC, and DhaB123, demonstrated activity with 1,2,4-butanetriol as a substrate, with GldABC and DhaB123 having the most significant activity (FIG. 4).

To examine 1,4-butanediol production, fresh transformants were grown overnight in LB at 37° C. Ampicillin (120 µg/L) and Kanamycin (50 µg/L) were added for plasmid maintenance. From these overnights, 100 µl were subcultured into 20 ml of fermentation media (per Liter: 20 g Bacto tryptone, 10 g Bacto yeast extract, 5 g NaCl, 3.75 g K₂HPO₄, 0.24 g MgSO₄, and 0.34 g thiamine hydrochloride). The cells were incubated at 37° C. until the cells reached an OD₆₀₀ ~0.4-0.6, at which point IPTG (1 mM), D-xylonic acid (2% wt/vol), and coenzyme B 12 (0.5 mg/L) were added to the cultures. The cultures were then grown at 30° C. at 250 rpm.

After 24 hr, 1,4-butanediol was observed for all of the strains expressing mdlC, yqhD/dadhA, and one of the diol dehydratases (gldABC, pddABC, or dhaB123) (FIG. 5). This production was not observed for the strain that did not contain the plasmids, nor for the strain expressing mdlC/yqhD, which did not express one of the diol dehydratases.

A number of embodiments of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other embodiments are within the scope of the following claims.

SEQUENCE LISTING

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<212> TYPE: DNA
<213> ORGANISM: Burkholderia fungorum
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(807)

<400> SEQUENCE: 1

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1 5 10 15	

gca atc tat ccc agc ctc tca ggc aaa acg gtt gtc atc acc ggc ggc	96
Ala Ile Tyr Pro Ser Leu Ser Gly Lys Thr Val Val Ile Thr Gly Gly	
20 25 30	

ggc agc ggc atc ggc gcc gcg atg gtc gaa gct ttc gcc cgg cag ggc	144
Gly Ser Gly Ile Gly Ala Ala Met Val Glu Ala Phe Ala Arg Gln Gly	

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35	40	45	
gcg cga gtt ttc ttc ctc gac gtc gct gag gac gat tcg ctg gcg ttg Ala Arg Val Phe Phe Leu Asp Val Ala Glu Asp Asp Ser Leu Ala Leu	50	55	192
50	60		
cag caa tcg ctg agc gac gcg cct cac ccg ccg ttg ttc cgc cgc tgc Gln Gln Ser Leu Ser Asp Ala Pro His Pro Pro Leu Phe Arg Arg Cys	65	70	240
65	75	80	
gat ctg cgc agc gtc gat gcg atc cac agt gcg ttt gcc ggg atc gtc Asp Leu Arg Ser Val Asp Ala Ile His Ser Ala Phe Ala Gly Ile Val	85	90	288
85	95		
gag atc gcc ggg ccg atc gag gta ctc gtc aac aac gct ggc aac gac Glu Ile Ala Gly Pro Ile Glu Val Leu Val Asn Asn Ala Gly Asn Asp	100	105	336
100	110		
gac cgg cat gaa gtc gac gcc atc acg ccg gcc tat tgg gac gag cgc Asp Arg His Glu Val Asp Ala Ile Thr Pro Ala Tyr Trp Asp Glu Arg	115	120	384
115	125		
atg gcc gtg aac ctg cgg cac cag ttc ttc tgc gcg cag gcc gca gcg Met Ala Val Asn Leu Arg His Gln Phe Phe Cys Ala Gln Ala Ala Ala	130	135	432
130	140		
gcc ggc atg cgc aag atc ggg cgc ggc gtg atc ctg aat ctt ggc tgc Ala Gly Met Arg Lys Ile Gly Arg Gly Val Ile Leu Asn Leu Gly Ser	145	150	480
145	155	160	
gtt tcc tgg cac ctc gcg ttg ccg aac ctc gcg atc tac atg agc gcg Val Ser Trp His Leu Ala Leu Pro Asn Leu Ala Ile Tyr Met Ser Ala	165	170	528
165	175		
aag gcc ggt atc gaa ggg ctg acc ccg ggc ctc gcg cgc gat ctc ggc Lys Ala Gly Ile Glu Gly Leu Thr Arg Gly Leu Ala Arg Asp Leu Gly	180	185	576
180	190		
gcc gcc ggc atc cgc gtg aac tgc att att ccc ggc gcg gtg cgg act Ala Ala Gly Ile Arg Val Asn Cys Ile Ile Pro Gly Ala Val Arg Thr	195	200	624
195	205		
ccc cgt cag atg cag ctc tgg cag tcg ccc gag agc gaa gcg aag ctc Pro Arg Gln Met Gln Leu Trp Gln Ser Pro Glu Ser Glu Ala Lys Leu	210	215	672
210	220		
gtc gcc agc caa tgt ctg cgt ttg cgt atc gaa cct gag cat gtc gcg Val Ala Ser Gln Cys Leu Arg Leu Arg Ile Glu Pro Glu His Val Ala	225	230	720
225	235	240	
cgc atg gcg ttg ttt ctt ccg tcc gac gat gcg tcg cgt tgc tca ggg Arg Met Ala Leu Phe Leu Ala Ser Asp Asp Ala Ser Arg Cys Ser Gly	245	250	768
245	255		
cgg gat tat ttc gtc gac gcc ggg ttg tac gga gaa tga Arg Asp Tyr Phe Val Asp Ala Gly Trp Tyr Gly Glu	260	265	807
260			

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<212> TYPE: PRT

<213> ORGANISM: Burkholderia fungorum

<400> SEQUENCE: 2

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1															

Ala	Ile	Tyr	Pro	Ser	Leu	Ser	Gly	Lys	Thr	Val	Val	Ile	Thr	Gly	Gly
20															

Gly	Ser	Gly	Ile	Gly	Ala	Ala	Met	Val	Glu	Ala	Phe	Ala	Arg	Gln	Gly
35															

Ala	Arg	Val	Phe	Phe	Leu	Asp	Val	Ala	Glu	Asp	Asp	Ser	Leu	Ala	Leu
50															

Gln Gln Ser Leu Ser Asp Ala Pro His Pro Pro Leu Phe Arg Arg Cys

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65	70	75	80
Asp Leu Arg Ser Val Asp Ala Ile His Ser Ala Phe Ala Gly Ile Val			
85	90	95	
Glu Ile Ala Gly Pro Ile Glu Val Leu Val Asn Asn Ala Gly Asn Asp			
100	105	110	
Asp Arg His Glu Val Asp Ala Ile Thr Pro Ala Tyr Trp Asp Glu Arg			
115	120	125	
Met Ala Val Asn Leu Arg His Gln Phe Phe Cys Ala Gln Ala Ala Ala			
130	135	140	
Ala Gly Met Arg Lys Ile Gly Arg Gly Val Ile Leu Asn Leu Gly Ser			
145	150	155	160
Val Ser Trp His Leu Ala Leu Pro Asn Leu Ala Ile Tyr Met Ser Ala			
165	170	175	
Lys Ala Gly Ile Glu Gly Leu Thr Arg Gly Leu Ala Arg Asp Leu Gly			
180	185	190	
Ala Ala Gly Ile Arg Val Asn Cys Ile Ile Pro Gly Ala Val Arg Thr			
195	200	205	
Pro Arg Gln Met Gln Leu Trp Gln Ser Pro Glu Ser Glu Ala Lys Leu			
210	215	220	
Val Ala Ser Gln Cys Leu Arg Leu Arg Ile Glu Pro Glu His Val Ala			
225	230	235	240
Arg Met Ala Leu Phe Leu Ala Ser Asp Asp Ala Ser Arg Cys Ser Gly			
245	250	255	
Arg Asp Tyr Phe Val Asp Ala Gly Trp Tyr Gly Glu			
260	265		

<210> SEQ_ID NO 3

<211> LENGTH: 747

<212> TYPE: DNA

<213> ORGANISM: Caulobacter crescentus

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(747)

<400> SEQUENCE: 3

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acc ggc ggc tcg ggc atc ggg gcc ggc ctc acc gcc ggc ttc gcc	96
Thr Gly Gly Ser Gly Ile Gly Ala Gly Leu Thr Ala Gly Phe Ala	
20 25 30	
cgt cag ggc gcg gag gtg atc ttc ctc gac atc gcc gac gag gac tcc	144
Arg Gln Gly Ala Glu Val Ile Phe Leu Asp Ile Ala Asp Glu Asp Ser	
35 40 45	
agg gct ctt gag gcc gag ctg gcc ggc tcg ccg atc ccg ccg gtc tac	192
Arg Ala Leu Glu Ala Glu Leu Ala Gly Ser Pro Ile Pro Pro Val Tyr	
50 55 60	
aag cgc tgc gac ctg atg aac ctc gag gcg atc aag gcg gtc ttc gcc	240
Lys Arg Cys Asp Leu Met Asn Leu Glu Ala Ile Lys Ala Val Phe Ala	
65 70 75 80	
gag atc ggc gac gtc gac gtg ctg gtc aac aac gcc ggc aat gac gac	288
Glu Ile Gly Asp Val Asp Val Leu Val Asn Asn Ala Gly Asn Asp Asp	
85 90 95	
cgc cac aag ctg gcc gac gtg acc ggc gcc tat tgg gac gag cgg atc	336
Arg His Lys Leu Ala Asp Val Thr Gly Ala Tyr Trp Asp Glu Arg Ile	
100 105 110	
aac gtc aac ctg cgc cac atg ctg ttc tgc acc cag gcc gtc gcg ccg	384
Asn Val Asn Leu Arg His Met Leu Phe Cys Thr Gln Ala Val Ala Pro	

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115	120	125	
ggc atg aag aag cgt ggc ggc ggg gcg gtg atc aac ttc ggt tcg atc Gly Met Lys Lys Arg Gly Gly Ala Val Ile Asn Phe Gly Ser Ile 130 135 140			432
agc tgg cac ctg ggg ctt gag gac ctc gtc ctc tac gaa acc gcc aag Ser Trp His Leu Gly Leu Glu Asp Leu Val Leu Tyr Glu Thr Ala Lys 145 150 155 160			480
gcc ggc atc gaa ggc atg acc cgc gcg ctg gcc cgg gag ctg ggt ccc Ala Gly Ile Glu Gly Met Thr Arg Ala Leu Ala Arg Glu Leu Gly Pro 165 170 175			528
gac gac atc cgc gtc acc tgc gtg ctc ggc aac gtc aag acc aag Asp Asp Ile Arg Val Thr Cys Val Val Pro Gly Asn Val Lys Thr Lys 180 185 190			576
cgc cag gag aag tgg tac acg ccc gaa ggc gag gcc cag atc gtg gcg Arg Gln Glu Lys Trp Tyr Thr Pro Glu Gly Glu Ala Gln Ile Val Ala 195 200 205			624
gcc caa tgc ctg aag ggc cgc atc gtc ccg gag aac gtc gcc gcg ctg Ala Gln Cys Leu Lys Gly Arg Ile Val Pro Glu Asn Val Ala Ala Leu 210 215 220			672
gtg ctg ttc ctg gcc tcg gat gac gcg tcg ctc tgc acc ggc cac gaa Val Leu Phe Leu Ala Ser Asp Asp Ala Ser Leu Cys Thr Gly His Glu 225 230 235 240			720
tac tgg atc gac gcc ggc tgg cgt tga Tyr Trp Ile Asp Ala Gly Trp Arg 245			747

<210> SEQ_ID NO 4

<211> LENGTH: 248

<212> TYPE: PRT

<213> ORGANISM: Caulobacter crescentus

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Arg Gln Gly Ala Glu Val Ile Phe Leu Asp Ile Ala Asp Glu Asp Ser 35 40 45		
Arg Ala Leu Glu Ala Glu Leu Ala Gly Ser Pro Ile Pro Pro Val Tyr 50 55 60		
Lys Arg Cys Asp Leu Met Asn Leu Glu Ala Ile Lys Ala Val Phe Ala 65 70 75 80		
Glu Ile Gly Asp Val Asp Val Leu Val Asn Asn Ala Gly Asn Asp Asp 85 90 95		
Arg His Lys Leu Ala Asp Val Thr Gly Ala Tyr Trp Asp Glu Arg Ile 100 105 110		
Asn Val Asn Leu Arg His Met Leu Phe Cys Thr Gln Ala Val Ala Pro 115 120 125		
Gly Met Lys Lys Arg Gly Gly Ala Val Ile Asn Phe Gly Ser Ile 130 135 140		
Ser Trp His Leu Gly Leu Glu Asp Leu Val Leu Tyr Glu Thr Ala Lys 145 150 155 160		
Ala Gly Ile Glu Gly Met Thr Arg Ala Leu Ala Arg Glu Leu Gly Pro 165 170 175		
Asp Asp Ile Arg Val Thr Cys Val Val Pro Gly Asn Val Lys Thr Lys 180 185 190		
Arg Gln Glu Lys Trp Tyr Thr Pro Glu Gly Glu Ala Gln Ile Val Ala		

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195	200	205
Ala Gln Cys Leu Lys Gly Arg Ile Val Pro Glu Asn Val Ala Ala Leu		
210	215	220
Val Leu Phe Leu Ala Ser Asp Asp Ala Ser Leu Cys Thr Gly His Glu		
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Tyr Trp Ile Asp Ala Gly Trp Arg		
245		

<210> SEQ ID NO 5

<211> LENGTH: 1968

<212> TYPE: DNA

<213> ORGANISM: Escherichia coli

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (1968)

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1 5 10 15	
gtg atc acc cac gcg ggg ccg cag ggc gct ctg ccg ctg acc ccg	96
Val Ile Thr His Ala Ala Gly Pro Gln Gly Ala Leu Pro Leu Thr Pro	
20 25 30	
cag atg ctg atg gaa tct ccc agc ggc aac ctg ttc ggc atg acg cag	144
Gln Met Leu Met Glu Ser Pro Ser Gly Asn Leu Phe Gly Met Thr Gln	
35 40 45	
aac gcc ggg atg ggc tgg gac gcc aac aag ctc acc ggc aaa gag gtg	192
Asn Ala Gly Met Gly Trp Asp Ala Asn Lys Leu Thr Gly Lys Glu Val	
50 55 60	
ctg att atc ggc act cag ggc ggc atc cgc gcc gga gac gga cgc cca	240
Leu Ile Ile Gly Thr Gln Gly Ile Arg Ala Gly Asp Gly Arg Pro	
65 70 75 80	
atc gcg ctg ggc tac cac acc ggg cat tgg gag atc ggc atg cag atg	288
Ile Ala Leu Gly Tyr His Thr Gly His Trp Glu Ile Gly Met Gln Met	
85 90 95	
cag gcg gcg aag gag atc acc cgc aat ggc ggg atc ccg ttc gcg	336
Gln Ala Ala Lys Glu Ile Thr Arg Asn Gly Ile Pro Phe Ala	
100 105 110	
gcc ttc gtc agc gat ccg tgc gac ggg cgc tcg cag ggc acg cac ggt	384
Ala Phe Val Ser Asp Pro Cys Asp Gly Arg Ser Gln Gly Thr His Gly	
115 120 125	
atg ttc gat tcc ctg tac cgc aac gac gcg gcg atc gtg ttt cgc	432
Met Phe Asp Ser Leu Pro Tyr Arg Asn Asp Ala Ala Ile Val Phe Arg	
130 135 140	
cgc ctg atc cgc tcc ctg ccg acg ccg cgg gcg gtg atc ggc gta gcg	480
Arg Leu Ile Arg Ser Leu Pro Thr Arg Arg Ala Val Ile Gly Val Ala	
145 150 155 160	
acc tgc gat aaa ggg ctg ccc gcc acc atg att gcg ctg gcc gcg atg	528
Thr Cys Asp Lys Gly Leu Pro Ala Thr Met Ile Ala Leu Ala Ala Met	
165 170 175	
cac gac ctg ccg act att ctg gtg ccg ggg ggc acg ctg ccg ccg	576
His Asp Leu Pro Thr Ile Leu Val Pro Gly Gly Ala Thr Leu Pro Pro	
180 185 190	
acc gtc ggg gaa gac gcg ggc aag gtg cag acc atc ggc gcg cgt ttc	624
Thr Val Gly Glu Asp Ala Gly Lys Val Gln Thr Ile Gly Ala Arg Phe	
195 200 205	
gcc aac cac gaa ctc tcc ctg cag gag gcc gcc gaa ctg ggc tgt cgc	672
Ala Asn His Glu Leu Ser Leu Gln Glu Ala Ala Glu Leu Gly Cys Arg	
210 215 220	
gcc tgc gcc tcc ccg ggc ggc ggg tgt cag ttc ctc ggc acg gcg ggc	720

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Ala Cys Ala Ser Pro Gly Gly Gly Cys Gln Phe Leu Gly Thr Ala Gly		
225	230	235
240		
acc tcg cag gtg gtc gcg gag gcg ctg ggt ctg gcg ctg ccg cac tcc		768
Thr Ser Gln Val Val Ala Glu Ala Leu Gly Leu Ala Leu Pro His Ser		
245	250	255
gcg ctg gcg ccg tcc ggg cag gcg gtg tgg ctg gag atc gcc ccg cag		816
Ala Leu Ala Pro Ser Gly Gln Ala Val Trp Leu Glu Ile Ala Arg Gln		
260	265	270
tgc gcg ccg gtc agc gag ctg gat agc ccg ggc atc acc acg ccg		864
Ser Ala Arg Ala Val Ser Glu Leu Asp Ser Arg Gly Ile Thr Thr Arg		
275	280	285
gat atc ctc tcc gat aaa gcc atc gaa aac gcg atg gtg atc cac gcg		912
Asp Ile Leu Ser Asp Lys Ala Ile Glu Asn Ala Met Val Ile His Ala		
290	295	300
gcg ttc ggc ggc tcc acc aat tta ctg ctg cac att ccg gcc atc gcc		960
Ala Phe Gly Gly Ser Thr Asn Leu Leu His Ile Pro Ala Ile Ala		
305	310	315
320		
cac gcg ggc tgc acg atc ccg gac gtt gag cac tgg acg ccg atc		1008
His Ala Ala Gly Cys Thr Ile Pro Asp Val Glu His Trp Thr Arg Ile		
325	330	335
aac cgt aaa gtg ccg cgt ctg gtg agc gtg ctg ccc aac ggc ccg gac		1056
Asn Arg Lys Val Pro Arg Leu Val Ser Val Leu Pro Asn Gly Pro Asp		
340	345	350
tat cac ccg acc gtg cgc gcc ttc ctc gcg ggc ggc gtg ccg gag gtg		1104
Tyr His Pro Thr Val Arg Ala Phe Leu Ala Gly Gly Val Pro Glu Val		
355	360	365
atg ctc cac ctg cgc gac ctc ggc ctg ctg cat ctg gac gcc atg acc		1152
Met Leu His Leu Arg Asp Leu Gly Leu Leu His Leu Asp Ala Met Thr		
370	375	380
gtg acc ggc cag acg gtg ggc gag aac ctt gaa tgg tgg cag gcg tcc		1200
Val Thr Gly Gln Thr Val Gly Glu Asn Leu Glu Trp Trp Gln Ala Ser		
385	390	395
400		
gag cgc cgg cgc ttc cgc cag tgc ctg cgc gag cag gac ggc gta		1248
Glu Arg Arg Ala Arg Phe Arg Gln Cys Leu Arg Glu Gln Asp Gly Val		
405	410	415
gag ccg gat gac gtg atc ctg ccg gag aag gca aaa gcg aaa ggg		1296
Glu Pro Asp Asp Val Ile Leu Pro Pro Glu Lys Ala Lys Ala Lys Gly		
420	425	430
ctg acc tcg acg gtc tgc ttc ccg acg ggc aac atc gct ccg gaa ggt		1344
Leu Thr Ser Thr Val Cys Phe Pro Thr Gly Asn Ile Ala Pro Glu Gly		
435	440	445
tcg gtg atc aag gcc acg gcg atc gac ccg tgc gtg gtg ggc gaa gat		1392
Ser Val Ile Lys Ala Thr Ala Ile Asp Pro Ser Val Val Gly Glu Asp		
450	455	460
ggc gta tac cac cac acc ggc cgg gtg cgg gtg ttt gtc tcg gaa gcg		1440
Gly Val Tyr His His Thr Gly Arg Val Arg Val Phe Val Ser Glu Ala		
465	470	475
480		
cag gcg atc aag gcg atc aag cgg gaa gag att gtg cag ggc gat atc		1488
Gln Ala Ile Lys Ala Ile Lys Arg Glu Glu Ile Val Gln Gly Asp Ile		
485	490	495
atg gtg gtg atc ggc ggc ggg ccg tcc ggc acc ggc atg gaa gag acc		1536
Met Val Val Ile Gly Gly Pro Ser Gly Thr Gly Met Glu Glu Thr		
500	505	510
tac cag ctc acc tcc ggc cta aag cat atc tcg tgg ggc aag acg gtg		1584
Tyr Gln Leu Thr Ser Ala Leu Lys His Ile Ser Trp Gly Lys Thr Val		
515	520	525
tcg ctc atc acc gat ggc cgc ttc tcg ggc gtg tcg acg ggc gcc tgc		1632
Ser Leu Ile Thr Asp Ala Arg Phe Ser Gly Val Ser Thr Gly Ala Cys		
530	535	540

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ttc ggc cac gtg tcg ccg gag ggc ctg gcg ggc ggg ccg att ggc aag Phe Gly His Val Ser Pro Glu Ala Leu Ala Gly Gly Pro Ile Gly Lys 545 550 555 560	1680
ctg cgc gat aac gac atc atc gag att gcc gtg gat cgt ctg acg tta Leu Arg Asp Asn Asp Ile Ile Glu Ile Ala Val Asp Arg Leu Thr Leu 565 570 575	1728
act ggc agc gtg aac ttc atc ggc acc ggc gac aac ccg ctg acg ccg Thr Gly Ser Val Asn Phe Ile Gly Thr Ala Asp Asn Pro Leu Thr Pro 580 585 590	1776
gaa gag ggc gcg cgc gag ctg gcg cgg cag acg cac ccg gac ctg Glu Glu Gly Ala Arg Glu Leu Ala Arg Arg Gln Thr His Pro Asp Leu 595 600 605	1824
cac gcc cac gac ttt ttg ccg gac acc ccg ctg tgg gca ctg His Ala His Asp Phe Leu Pro Asp Asp Thr Arg Leu Trp Ala Ala Leu 610 615 620	1872
cag tcg gtg agc ggc ggc acc tgg aaa ggc tgt att tat gac acc gat Gln Ser Val Ser Gly Gly Thr Trp Lys Gly Cys Ile Tyr Asp Thr Asp 625 630 635 640	1920
aaa att atc gag gta att aac gcc ggt aaa aaa ggc ctc gga att taa Lys Ile Ile Glu Val Ile Asn Ala Gly Lys Lys Ala Leu Gly Ile 645 650 655	1968

<210> SEQ_ID NO 6

<211> LENGTH: 655

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 6

Met Thr Ile Glu Lys Ile Phe Thr Pro Gln Asp Asp Ala Phe Tyr Ala
1 5 10 15

Val Ile Thr His Ala Ala Gly Pro Gln Gly Ala Leu Pro Leu Thr Pro
20 25 30

Gln Met Leu Met Glu Ser Pro Ser Gly Asn Leu Phe Gly Met Thr Gln
35 40 45

Asn Ala Gly Met Gly Trp Asp Ala Asn Lys Leu Thr Gly Lys Glu Val
50 55 60

Leu Ile Ile Gly Thr Gln Gly Ile Arg Ala Gly Asp Gly Arg Pro
65 70 75 80

Ile Ala Leu Gly Tyr His Thr Gly His Trp Glu Ile Gly Met Gln Met
85 90 95

Gln Ala Ala Ala Lys Glu Ile Thr Arg Asn Gly Gly Ile Pro Phe Ala
100 105 110

Ala Phe Val Ser Asp Pro Cys Asp Gly Arg Ser Gln Gly Thr His Gly
115 120 125

Met Phe Asp Ser Leu Pro Tyr Arg Asn Asp Ala Ala Ile Val Phe Arg
130 135 140

Arg Leu Ile Arg Ser Leu Pro Thr Arg Arg Ala Val Ile Gly Val Ala
145 150 155 160

Thr Cys Asp Lys Gly Leu Pro Ala Thr Met Ile Ala Leu Ala Ala Met
165 170 175

His Asp Leu Pro Thr Ile Leu Val Pro Gly Gly Ala Thr Leu Pro Pro
180 185 190

Thr Val Gly Glu Asp Ala Gly Lys Val Gln Thr Ile Gly Ala Arg Phe
195 200 205

Ala Asn His Glu Leu Ser Leu Gln Glu Ala Ala Glu Leu Gly Cys Arg
210 215 220

Ala Cys Ala Ser Pro Gly Gly Cys Gln Phe Leu Gly Thr Ala Gly

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225	230	235	240
Thr Ser Gln Val Val Ala Glu Ala Leu Gly Leu Ala Leu Pro His Ser			
245	250	255	
Ala Leu Ala Pro Ser Gly Gln Ala Val Trp Leu Glu Ile Ala Arg Gln			
260	265	270	
Ser Ala Arg Ala Val Ser Glu Leu Asp Ser Arg Gly Ile Thr Thr Arg			
275	280	285	
Asp Ile Leu Ser Asp Lys Ala Ile Glu Asn Ala Met Val Ile His Ala			
290	295	300	
Ala Phe Gly Gly Ser Thr Asn Leu Leu Leu His Ile Pro Ala Ile Ala			
305	310	315	320
His Ala Ala Gly Cys Thr Ile Pro Asp Val Glu His Trp Thr Arg Ile			
325	330	335	
Asn Arg Lys Val Pro Arg Leu Val Ser Val Leu Pro Asn Gly Pro Asp			
340	345	350	
Tyr His Pro Thr Val Arg Ala Phe Leu Ala Gly Gly Val Pro Glu Val			
355	360	365	
Met Leu His Leu Arg Asp Leu Gly Leu Leu His Leu Asp Ala Met Thr			
370	375	380	
Val Thr Gly Gln Thr Val Gly Glu Asn Leu Glu Trp Trp Gln Ala Ser			
385	390	395	400
Glu Arg Arg Ala Arg Phe Arg Gln Cys Leu Arg Glu Gln Asp Gly Val			
405	410	415	
Glu Pro Asp Asp Val Ile Leu Pro Pro Glu Lys Ala Lys Ala Lys Gly			
420	425	430	
Leu Thr Ser Thr Val Cys Phe Pro Thr Gly Asn Ile Ala Pro Glu Gly			
435	440	445	
Ser Val Ile Lys Ala Thr Ala Ile Asp Pro Ser Val Val Gly Glu Asp			
450	455	460	
Gly Val Tyr His His Thr Gly Arg Val Arg Val Phe Val Ser Glu Ala			
465	470	475	480
Gln Ala Ile Lys Ala Ile Lys Arg Glu Glu Ile Val Gln Gly Asp Ile			
485	490	495	
Met Val Val Ile Gly Gly Pro Ser Gly Thr Gly Met Glu Glu Thr			
500	505	510	
Tyr Gln Leu Thr Ser Ala Leu Lys His Ile Ser Trp Gly Lys Thr Val			
515	520	525	
Ser Leu Ile Thr Asp Ala Arg Phe Ser Gly Val Ser Thr Gly Ala Cys			
530	535	540	
Phe Gly His Val Ser Pro Glu Ala Leu Ala Gly Gly Pro Ile Gly Lys			
545	550	555	560
Leu Arg Asp Asn Asp Ile Ile Glu Ile Ala Val Asp Arg Leu Thr Leu			
565	570	575	
Thr Gly Ser Val Asn Phe Ile Gly Thr Ala Asp Asn Pro Leu Thr Pro			
580	585	590	
Glu Glu Gly Ala Arg Glu Leu Ala Arg Arg Gln Thr His Pro Asp Leu			
595	600	605	
His Ala His Asp Phe Leu Pro Asp Asp Thr Arg Leu Trp Ala Ala Leu			
610	615	620	
Gln Ser Val Ser Gly Gly Thr Trp Lys Gly Cys Ile Tyr Asp Thr Asp			
625	630	635	640
Lys Ile Ile Glu Val Ile Asn Ala Gly Lys Lys Ala Leu Gly Ile			
645	650	655	

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<210> SEQ_ID NO 7
<211> LENGTH: 1968
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1968)

<400> SEQUENCE: 7

atg tct gtt cgc aat att ttt gct gac gag agc cac gat att tac acc	48
Met Ser Val Arg Asn Ile Phe Ala Asp Glu Ser His Asp Ile Tyr Thr	
1 5 10 15	
gtc aga acg cac gcc gat ggc ccg gac gga ctc cca tta acc gca	96
Val Arg Thr His Ala Asp Gly Pro Asp Gly Glu Leu Pro Leu Thr Ala	
20 25 30	
gag atg ctt atc aac cgc ccg agc ggg gat ctg ttc ggt atg acc atg	144
Glu Met Leu Ile Asn Arg Pro Ser Gly Asp Leu Phe Gly Met Thr Met	
35 40 45	
aat gcc gga atg ggt tgg tct ccg gac gag ctg gat cgg gac ggt att	192
Asn Ala Gly Met Gly Trp Ser Pro Asp Glu Leu Asp Arg Asp Gly Ile	
50 55 60	
tta ctg ctc agt aca ctc ggt ggc tta cgc ggc gca gac ggt aaa ccc	240
Leu Leu Leu Ser Thr Leu Gly Gly Leu Arg Gly Ala Asp Gly Lys Pro	
65 70 75 80	
gtg gcg ctg gcg ttg cac cag ggg cat tac gaa ctg gac atc cag atg	288
Val Ala Leu Ala Leu His Gln Gly His Tyr Glu Leu Asp Ile Gln Met	
85 90 95	
aaa gcg gcg gcc gag gtt att aaa gcc aac cat gcc ctg ccc tat gcc	336
Lys Ala Ala Ala Glu Val Ile Lys Ala Asn His Ala Leu Pro Tyr Ala	
100 105 110	
gtg tac gtc tcc gat cct tgt gac ggg cgt act cag ggt aca acg ggg	384
Val Tyr Val Ser Asp Pro Cys Asp Gly Arg Thr Gln Gly Thr Thr Gly	
115 120 125	
atg ttt gat tcg cta cca tac cga aat gac gca tcg atg gta atg cgc	432
Met Phe Asp Ser Leu Pro Tyr Arg Asn Asp Ala Ser Met Val Met Arg	
130 135 140	
cgc ctt att cgc tct ctg ccc gac gcg aaa gca gtt att ggt gtg gcg	480
Arg Leu Ile Arg Ser Leu Pro Asp Ala Lys Ala Val Ile Gly Val Ala	
145 150 155 160	
agt tgc gat aag ggg ctt ccg gcc acc atg atg gca ctc gcc gcg cag	528
Ser Cys Asp Lys Gly Leu Pro Ala Thr Met Met Ala Leu Ala Ala Gln	
165 170 175	
cac aac atc gca acc gtg ctg gtc ccc ggc ggc gcg acg ctg ccc gca	576
His Asn Ile Ala Thr Val Leu Val Pro Gly Gly Ala Thr Leu Pro Ala	
180 185 190	
aag gat gga gaa gac aac ggc aag gtgcaa acc att ggc gca cgc ttc	624
Lys Asp Gly Glu Asp Asn Gly Lys Val Gln Thr Ile Gly Ala Arg Phe	
195 200 205	
gcc aat ggc gaa tta tct cta cag gac gca cgc cgt gcg ggc tgt aaa	672
Ala Asn Gly Glu Leu Ser Leu Gln Asp Ala Arg Arg Ala Gly Cys Lys	
210 215 220	
gcc tgt gcc tct tcc ggc ggc ggc tgt caa ttt ttg ggc act gcc ggg	720
Ala Cys Ala Ser Ser Gly Gly Gly Cys Gln Phe Leu Gly Thr Ala Gly	
225 230 235 240	
aca tct cag gtg gtg gcc gaa gga ttg gga ctg gca atc cca cat tca	768
Thr Ser Gln Val Val Ala Glu Gly Leu Ala Ile Pro His Ser	
245 250 255	
gcc ctg gcc cct tcc ggt gag cct gtg tgg cgg gag atc gcc aga gct	816
Ala Leu Ala Pro Ser Gly Glu Pro Val Trp Arg Glu Ile Ala Arg Ala	
260 265 270	

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tcc gcg cga gct gcg ctg aac ctg agt caa aaa ggc atc acc acc acc cg	864
Ser Ala Arg Ala Ala Leu Asn Leu Ser Gln Lys Gly Ile Thr Thr Arg	
275 280 285	
gaa att ctc acc gat aaa gcg ata gag aat gcg atg acg gtc cat gcc	912
Glu Ile Leu Thr Asp Lys Ala Ile Glu Asn Ala Met Thr Val His Ala	
290 295 300	
gcg ttc ggt ggt tca aca aac ctg ctg tta cac atc ccg gca att gct	960
Ala Phe Gly Gly Ser Thr Asn Leu Leu His Ile Pro Ala Ile Ala	
305 310 315 320	
cac cag gca ggt tgc cat atc ccg acc gtt gat gac tgg atc cgc atc	1008
His Gln Ala Gly Cys His Ile Pro Thr Val Asp Asp Trp Ile Arg Ile	
325 330 335	
aac aag cgc gtg ccc cga ctg gtg agc gta ctg cct aat ggc ccg gtt	1056
Asn Lys Arg Val Pro Arg Leu Val Ser Val Leu Pro Asn Gly Pro Val	
340 345 350	
tat cat cca acg gtc aat gcc ttt atg gca ggt ggt gtg ccg gaa gtc	1104
Tyr His Pro Thr Val Asn Ala Phe Met Ala Gly Gly Val Pro Glu Val	
355 360 365	
atg ttg cat ctg cgc agc ctc gga ttg ttg cat gaa gac gtt atg acg	1152
Met Leu His Leu Arg Ser Leu Gly Leu Leu His Glu Asp Val Met Thr	
370 375 380	
gtt acc ggc agc acg ctg aaa gaa aac ctc gac tgg tgg gag cac tcc	1200
Val Thr Gly Ser Thr Leu Lys Glu Asn Leu Asp Trp Trp Glu His Ser	
385 390 395 400	
gaa cgg cgt cag cgg ttc aag caa ctc ctg ctc gat cag gaa caa atc	1248
Glu Arg Arg Gln Arg Phe Lys Gln Leu Leu Asp Gln Glu Gln Ile	
405 410 415	
aac gct gac gaa gtg atc atg tct ccg cag caa gca aaa gcg cgc gga	1296
Asn Ala Asp Glu Val Ile Met Ser Pro Gln Gln Ala Lys Ala Arg Gly	
420 425 430	
tta acc tca act atc acc ttc ccg gtg ggc aat att gcg cca gaa ggt	1344
Leu Thr Ser Thr Ile Thr Phe Pro Val Gly Asn Ile Ala Pro Glu Gly	
435 440 445	
tcg gtg atc aaa tcc acc gcc att gac ccc tcg atg att gat gag caa	1392
Ser Val Ile Lys Ser Thr Ala Ile Asp Pro Ser Met Ile Asp Glu Gln	
450 455 460	
ggt atc tat tac cat aaa ggt gtg gcg aag gtt tat ctg tcc gag aaa	1440
Gly Ile Tyr Tyr His Lys Gly Val Ala Lys Val Tyr Leu Ser Glu Lys	
465 470 475 480	
agt gcg att tac gat atc aaa cat gac aag atc aag gcg ggc gat att	1488
Ser Ala Ile Tyr Asp Ile Lys His Asp Lys Ile Lys Ala Gly Asp Ile	
485 490 495	
ctg gtc att att ggc gtt gga cct tca ggt aca ggg atg gaa gaa acc	1536
Leu Val Ile Ile Gly Val Gly Pro Ser Gly Thr Gly Met Glu Glu Thr	
500 505 510	
tac cag gtt acc agt gcc ctg aag cat ctg tca tac ggt aag cat gtt	1584
Tyr Gln Val Thr Ser Ala Leu Lys His Leu Ser Tyr Gly Lys His Val	
515 520 525	
tcg tta atc acc gat gca cgt ttc tcg ggc gtt tct act ggc gcg tgc	1632
Ser Leu Ile Thr Asp Ala Arg Phe Ser Gly Val Ser Thr Gly Ala Cys	
530 535 540	
atc ggc cat gtg ggg cca gaa gcg ctg gcc gga ggc ccc atc ggt aaa	1680
Ile Gly His Val Gly Pro Glu Ala Leu Ala Gly Gly Pro Ile Gly Lys	
545 550 555 560	
tta cgc acc ggg gat tta att gaa att aaa att gat tgt cgc gag ctt	1728
Leu Arg Thr Gly Asp Leu Ile Glu Ile Lys Ile Asp Cys Arg Glu Leu	
565 570 575	
cac ggc gaa gtc aat ttc ctc gga acc cgt agc gat gaa caa tta cct	1776
His Gly Glu Val Asn Phe Leu Gly Thr Arg Ser Asp Glu Gln Leu Pro	

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580	585	590	
tca cag gag gag gca act gca ata tta aat gcc aga ccc agc cat cag Ser Gln Glu Glu Ala Thr Ala Ile Leu Asn Ala Arg Pro Ser His Gln 595 600 605			1824
gat tta ctt ccc gat cct gaa ttg cca gat gat acc cgg cta tgg gca Asp Leu Leu Pro Asp Pro Glu Leu Pro Asp Asp Thr Arg Leu Trp Ala 610 615 620			1872
atg ctt cag gcc gtg agt ggt ggg aca tgg acc ggt tgt att tat gat Met Leu Gln Ala Val Ser Gly Gly Thr Trp Thr Gly Cys Ile Tyr Asp 625 630 635 640			1920
gta aac aaa att ggc gcg gct ttg cgc gat ttt atg aat aaa aac tga Val Asn Lys Ile Gly Ala Ala Leu Arg Asp Phe Met Asn Lys Asn 645 650 655			1968
 <210> SEQ_ID NO 8 <211> LENGTH: 655 <212> TYPE: PRT <213> ORGANISM: Escherichia coli			
 <400> SEQUENCE: 8			
Met Ser Val Arg Asn Ile Phe Ala Asp Glu Ser His Asp Ile Tyr Thr 1 5 10 15			
Val Arg Thr His Ala Asp Gly Pro Asp Gly Glu Leu Pro Leu Thr Ala 20 25 30			
Glu Met Leu Ile Asn Arg Pro Ser Gly Asp Leu Phe Gly Met Thr Met 35 40 45			
Asn Ala Gly Met Gly Trp Ser Pro Asp Glu Leu Asp Arg Asp Gly Ile 50 55 60			
Leu Leu Leu Ser Thr Leu Gly Gly Leu Arg Gly Ala Asp Gly Lys Pro 65 70 75 80			
Val Ala Leu Ala Leu His Gln Gly His Tyr Glu Leu Asp Ile Gln Met 85 90 95			
Lys Ala Ala Ala Glu Val Ile Lys Ala Asn His Ala Leu Pro Tyr Ala 100 105 110			
Val Tyr Val Ser Asp Pro Cys Asp Gly Arg Thr Gln Gly Thr Thr Gly 115 120 125			
Met Phe Asp Ser Leu Pro Tyr Arg Asn Asp Ala Ser Met Val Met Arg 130 135 140			
Arg Leu Ile Arg Ser Leu Pro Asp Ala Lys Ala Val Ile Gly Val Ala 145 150 155 160			
Ser Cys Asp Lys Gly Leu Pro Ala Thr Met Met Ala Leu Ala Ala Gln 165 170 175			
His Asn Ile Ala Thr Val Leu Val Pro Gly Gly Ala Thr Leu Pro Ala 180 185 190			
Lys Asp Gly Glu Asp Asn Gly Lys Val Gln Thr Ile Gly Ala Arg Phe 195 200 205			
Ala Asn Gly Glu Leu Ser Leu Gln Asp Ala Arg Arg Ala Gly Cys Lys 210 215 220			
Ala Cys Ala Ser Ser Gly Gly Cys Gln Phe Leu Gly Thr Ala Gly 225 230 235 240			
Thr Ser Gln Val Val Ala Glu Gly Leu Gly Leu Ala Ile Pro His Ser 245 250 255			
Ala Leu Ala Pro Ser Gly Glu Pro Val Trp Arg Glu Ile Ala Arg Ala 260 265 270			
Ser Ala Arg Ala Ala Leu Asn Leu Ser Gln Lys Gly Ile Thr Thr Arg 275 280 285			

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Glu Ile Leu Thr Asp Lys Ala Ile Glu Asn Ala Met Thr Val His Ala
 290 295 300
 Ala Phe Gly Gly Ser Thr Asn Leu Leu Leu His Ile Pro Ala Ile Ala
 305 310 315 320
 His Gln Ala Gly Cys His Ile Pro Thr Val Asp Asp Trp Ile Arg Ile
 325 330 335
 Asn Lys Arg Val Pro Arg Leu Val Ser Val Leu Pro Asn Gly Pro Val
 340 345 350
 Tyr His Pro Thr Val Asn Ala Phe Met Ala Gly Gly Val Pro Glu Val
 355 360 365
 Met Leu His Leu Arg Ser Leu Gly Leu Leu His Glu Asp Val Met Thr
 370 375 380
 Val Thr Gly Ser Thr Leu Lys Glu Asn Leu Asp Trp Trp Glu His Ser
 385 390 395 400
 Glu Arg Arg Gln Arg Phe Lys Gln Leu Leu Asp Gln Glu Gln Ile
 405 410 415
 Asn Ala Asp Glu Val Ile Met Ser Pro Gln Gln Ala Lys Ala Arg Gly
 420 425 430
 Leu Thr Ser Thr Ile Thr Phe Pro Val Gly Asn Ile Ala Pro Glu Gly
 435 440 445
 Ser Val Ile Lys Ser Thr Ala Ile Asp Pro Ser Met Ile Asp Glu Gln
 450 455 460
 Gly Ile Tyr Tyr His Lys Gly Val Ala Lys Val Tyr Leu Ser Glu Lys
 465 470 475 480
 Ser Ala Ile Tyr Asp Ile Lys His Asp Lys Ile Lys Ala Gly Asp Ile
 485 490 495
 Leu Val Ile Ile Gly Val Gly Pro Ser Gly Thr Gly Met Glu Glu Thr
 500 505 510
 Tyr Gln Val Thr Ser Ala Leu Lys His Leu Ser Tyr Gly Lys His Val
 515 520 525
 Ser Leu Ile Thr Asp Ala Arg Phe Ser Gly Val Ser Thr Gly Ala Cys
 530 535 540
 Ile Gly His Val Gly Pro Glu Ala Leu Ala Gly Gly Pro Ile Gly Lys
 545 550 555 560
 Leu Arg Thr Gly Asp Leu Ile Glu Ile Lys Ile Asp Cys Arg Glu Leu
 565 570 575
 His Gly Glu Val Asn Phe Leu Gly Thr Arg Ser Asp Glu Gln Leu Pro
 580 585 590
 Ser Gln Glu Ala Thr Ala Ile Leu Asn Ala Arg Pro Ser His Gln
 595 600 605
 Asp Leu Leu Pro Asp Pro Glu Leu Pro Asp Asp Thr Arg Leu Trp Ala
 610 615 620
 Met Leu Gln Ala Val Ser Gly Gly Thr Trp Thr Gly Cys Ile Tyr Asp
 625 630 635 640
 Val Asn Lys Ile Gly Ala Ala Leu Arg Asp Phe Met Asn Lys Asn
 645 650 655

<210> SEQ_ID NO 9

<211> LENGTH: 528

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas pudita

<400> SEQUENCE: 9

Met Ala Ser Val His Gly Thr Thr Tyr Glu Leu Leu Arg Arg Gln Gly

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1	5	10	15
Ile Asp Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu			
20	25	30	
Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Ala Leu Gln Glu Ala			
35	40	45	
Cys Val Val Gly Ile Ala Asp Gly Tyr Ala Gln Ala Ser Arg Lys Pro			
50	55	60	
Ala Phe Ile Asn Leu His Ser Ala Ala Gly Thr Gly Asn Ala Met Gly			
65	70	75	80
Ala Leu Ser Asn Ala Trp Asn Ser His Ser Pro Leu Ile Val Thr Ala			
85	90	95	
Gly Gln Gln Thr Arg Ala Met Ile Gly Val Glu Ala Leu Leu Thr Asn			
100	105	110	
Val Asp Ala Ala Asn Leu Pro Arg Pro Leu Val Lys Trp Ser Tyr Glu			
115	120	125	
Pro Ala Ser Ala Ala Glu Val Pro His Ala Met Ser Arg Ala Ile His			
130	135	140	
Met Ala Ser Met Ala Pro Gln Gly Pro Val Tyr Leu Ser Val Pro Tyr			
145	150	155	160
Asp Asp Trp Asp Lys Asp Ala Asp Pro Gln Ser His His Leu Phe Asp			
165	170	175	
Arg His Val Ser Ser Ser Val Arg Leu Asn Asp Gln Asp Leu Asp Ile			
180	185	190	
Leu Val Lys Ala Leu Asn Ser Ala Ser Asn Pro Ala Ile Val Leu Gly			
195	200	205	
Pro Asp Val Asp Ala Ala Asn Ala Asn Ala Asp Cys Val Met Leu Ala			
210	215	220	
Glu Arg Leu Lys Ala Pro Val Trp Val Ala Pro Ser Ala Pro Arg Cys			
225	230	235	240
Pro Phe Pro Thr Arg His Pro Cys Phe Arg Gly Leu Met Pro Ala Gly			
245	250	255	
Ile Ala Ala Ile Ser Gln Leu Leu Glu Gly His Asp Val Val Leu Val			
260	265	270	
Ile Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Asp Pro Gly Gln Tyr			
275	280	285	
Leu Lys Pro Gly Thr Arg Leu Ile Ser Val Thr Cys Asp Pro Leu Glu			
290	295	300	
Ala Ala Arg Ala Pro Met Gly Asp Ala Ile Val Ala Asp Ile Gly Ala			
305	310	315	320
Met Ala Ser Ala Leu Ala Asn Leu Val Glu Glu Ser Ser Arg Gln Leu			
325	330	335	
Pro Thr Ala Ala Pro Glu Pro Ala Lys Val Asp Gln Asp Ala Gly Arg			
340	345	350	
Leu His Pro Glu Thr Val Phe Asp Thr Leu Asn Asp Met Ala Pro Glu			
355	360	365	
Asn Ala Ile Tyr Leu Asn Glu Ser Thr Ser Thr Ala Gln Met Trp			
370	375	380	
Gln Arg Leu Asn Met Arg Asn Pro Gly Ser Tyr Tyr Phe Cys Ala Ala			
385	390	395	400
Gly Gly Leu Gly Phe Ala Leu Pro Ala Ala Ile Gly Val Gln Leu Ala			
405	410	415	
Glu Pro Glu Arg Gln Val Ile Ala Val Ile Gly Asp Gly Ser Ala Asn			
420	425	430	

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Tyr Ser Ile Ser Ala Leu Trp Thr Ala Ala Gln Tyr Asn Ile Pro Thr
435 440 445

Ile Phe Val Ile Met Asn Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
450 455 460

Ala Gly Val Leu Glu Ala Glu Asn Val Pro Gly Leu Asp Val Pro Gly
465 470 475 480

Ile Asp Phe Arg Ala Leu Ala Lys Gly Tyr Gly Val Gln Ala Leu Lys
485 490 495

Ala Asp Asn Leu Glu Gln Leu Lys Gly Ser Leu Gln Glu Ala Leu Ser
500 505 510

Ala Lys Gly Pro Val Leu Ile Glu Val Ser Thr Val Ser Pro Val Lys
515 520 525

<210> SEQ ID NO 10

<211> LENGTH: 346

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 10

Met Gln Asn Ile Ile Arg Lys Gly Gly Thr Met Lys Ala Ala Val Val
1 5 10 15

Thr Lys Asp His His Val Asp Val Thr Tyr Lys Thr Leu Arg Ser Leu
20 25 30

Lys His Gly Glu Ala Leu Leu Lys Met Glu Cys Cys Gly Val Cys His
35 40 45

Thr Asp Leu His Val Lys Asn Gly Asp Phe Gly Asp Lys Thr Gly Val
50 55 60

Ile Leu Gly His Glu Gly Ile Gly Val Val Ala Glu Val Gly Pro Gly
65 70 75 80

Val Thr Ser Leu Lys Pro Gly Asp Arg Ala Ser Val Ala Trp Phe Tyr
85 90 95

Glu Gly Cys Gly His Cys Glu Tyr Cys Asn Ser Gly Asn Glu Thr Leu
100 105 110

Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser Val Asp Gly Gly Met Ala
115 120 125

Glu Glu Cys Ile Val Val Ala Asp Tyr Ala Val Lys Val Pro Asp Gly
130 135 140

Leu Asp Ser Ala Ala Ala Ser Ser Ile Thr Cys Ala Gly Val Thr Thr
145 150 155 160

Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg Pro Gly Gln Trp Ile Ala
165 170 175

Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu Ala Leu Gln Tyr Ala Lys
180 185 190

Asn Val Phe Asn Ala Lys Val Ile Ala Ile Asp Val Asn Asp Glu Gln
195 200 205

Leu Lys Leu Ala Thr Glu Met Gly Ala Asp Leu Ala Ile Asn Ser His
210 215 220

Thr Glu Asp Ala Ala Lys Ile Val Gln Glu Lys Thr Gly Gly Ala His
225 230 235 240

Ala Ala Val Val Thr Ala Val Ala Lys Ala Ala Phe Asn Ser Ala Val
245 250 255

Asp Ala Val Arg Ala Gly Gly Arg Val Val Ala Val Gly Leu Pro Pro
260 265 270

Glu Ser Met Ser Leu Asp Ile Pro Arg Leu Val Leu Asp Gly Ile Glu

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275 280 285

Val Val Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Thr Glu Ala Phe
 290 295 300

Gln Phe Ala Ala Glu Gly Lys Val Val Pro Lys Val Ala Leu Arg Pro
 305 310 315 320

Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu Met Glu Glu Gly Lys Ile
 325 330 335

Arg Gly Arg Met Val Ile Asp Phe Arg His
 340 345

<210> SEQ_ID NO 11

<211> LENGTH: 360

<212> TYPE: PRT

<213> ORGANISM: Haloarcula marismortui

<400> SEQUENCE: 11

Met Asn Val Asp Ala Leu Thr Gly Gly Phe Asp Arg Arg Asp Trp Gln
 1 5 10 15

Glu Gln Thr Ala Thr Asp Asn Pro Val Arg Phe Ala Met Ile Gly Val
 20 25 30

Gly Trp Trp Thr Thr Glu Gln Ala Met Pro Ala Val Asp Ala Gly Asp
 35 40 45

Leu Cys Glu Thr Thr Val Leu Val Ser Ser Asp Arg Glu Lys Ala Ala
 50 55 60

Asp Val Ala Ala Asp Ser Glu Thr Val Glu His Ala Ile Thr Tyr Glu
 65 70 75 80

Glu Phe His Asp Gly Ala Ala Ser Asp Ala Tyr Asp Ala Val Tyr Ile
 85 90 95

Val Thr Pro Asn Ala Leu His Leu Pro Tyr Val Glu Thr Ala Ala Glu
 100 105 110

Leu Asp Lys Ala Ile Leu Cys Glu Lys Pro Met Glu Ala Thr Ile Glu
 115 120 125

Arg Ala Glu Arg Met Val Glu Val Cys Asp Glu His Asp Ala Thr Leu
 130 135 140

Met Ile Ala Tyr Arg Met His Thr Glu Pro Ala Val Arg Arg Ala Lys
 145 150 155 160

Asp Leu Ile Asp Glu Gly Tyr Ile Gly Glu Pro Leu Phe Val His Gly
 165 170 175

Asn Met Thr Glu Pro Ile Leu Glu Leu Val Pro Asp Pro Asp Gln Trp
 180 185 190

Arg Leu Asp Gly Glu Leu Ser Gly Gly Cys Ala Val Met Asp Ile Gly
 195 200 205

Ile Tyr Pro Leu Asn Thr Ser Arg Phe Leu Leu Asp Ala Asp Pro Val
 210 215 220

Ala Val Arg Gly Thr Val Ala Ser Val Gln Glu Glu Phe Ala Asp Val
 225 230 235 240

Pro Asp Glu His Gly Ala Phe Gln Leu Asp Phe Pro Gly His Val Tyr
 245 250 255

Ala Val Cys Thr Ala Ser Gln Asn Ala His Leu Asp Ser His Ile Ser
 260 265 270

Val Leu Gly Thr Glu Gly Lys Val Arg Val Glu Pro Ala Phe Tyr Pro
 275 280 285

Trp Asp Asp Arg Ala Leu Gln Leu Ser His Glu Gly Thr Thr Val Glu
 290 295 300

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Ile Asp Phe Glu Gln Ile Asp Gln Met Glu Glu Glu Phe Glu Tyr Phe
 305 310 315 320

Ala His Cys Leu Leu Thr Asp Thr Glu Pro Tyr Ala Asp Gly Glu His
 325 330 335

Gly Leu Val Asp Ile Asn Thr Ile Lys Ser Val Tyr Glu Ala Ser Glu
 340 345 350

Thr Glu Ser Thr Val Arg Leu Asp
 355 360

<210> SEQ ID NO 12

<211> LENGTH: 357

<212> TYPE: PRT

<213> ORGANISM: Haloferax volcanii

<400> SEQUENCE: 12

Met Ser Leu Glu Ala Phe Leu Asp Asp Phe Glu Arg Arg Asn Trp Gln
 1 5 10 15

Arg Val Ser Asp Gly Thr Val Arg Ile Ala Val Ile Gly Leu Gly Trp
 20 25 30

Trp Thr Val Asp Gln Ala Ile Pro Ala Ile Asp Ala Ser Gly Leu Cys
 35 40 45

Glu Thr Thr Val Thr Val Ser Ser Thr Ser Glu Lys Ala Lys Arg Val
 50 55 60

Ala Ala Gly Val Glu Thr Ala Thr His Gly Leu Ser Tyr Asp Glu Phe
 65 70 75 80

His Ala Gly Glu Ala Ala Asp Ala Tyr Asp Ala Val Tyr Ile Cys Ser
 85 90 95

Pro Asn Ala Leu His Leu Pro Tyr Ala Arg Thr Ala Ala Glu Leu Gly
 100 105 110

Lys Ala Val Leu Cys Glu Lys Pro Ile Glu Ala Ser Ser Glu Arg Gly
 115 120 125

Gln Gln Met Val Asp Ala Cys Asp Glu Ala Gly Val Pro Leu Ile Val
 130 135 140

Gly Tyr Arg Met His Thr Glu Pro Ala Ile Arg Arg Ala Arg Lys Leu
 145 150 155 160

Ile Arg Asp Gly Val Ile Gly Asp Pro Val His Ala Ile Gly Thr Asn
 165 170 175

Ser Gln Ala Met Leu Glu Leu Ile Ser Asp Pro Asn Gln Trp Arg Leu
 180 185 190

Asp Pro Glu Leu Ala Gly Pro Gly Ala Thr Val Thr Asp Ile Gly Ile
 195 200 205

Tyr Pro Leu Asn Thr Cys Arg Phe Leu Leu Asp Ser Asp Pro Val Ala
 210 215 220

Ala Gln Ala Phe Met Gln Ser Ser His Asp Ala Phe Asp Gln Val Pro
 225 230 235 240

Asp Glu His Ser Ser Phe Met Val Glu Phe Asp Asp Gly Thr Tyr Leu
 245 250 255

Ala Ala Thr Ala Ser Gln Asn Ala Gln Ala Thr Thr Ser Leu Arg Ile
 260 265 270

Val Gly Thr Asn Gly Glu Ile Leu Val Glu Pro Ala Phe His Met Glu
 275 280 285

Thr Glu Ile Arg Val Thr Arg Asp Asp Val Ser Val Thr Leu Asp Thr
 290 295 300

Pro Gln Val Asn Gln Met Thr Glu Leu Phe Asp Tyr Ala Ala Asp Arg
 305 310 315 320

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Ile Leu Thr Asp Ala Pro Ile Gly Pro Asp Gly Glu His Gly Val Leu
 325 330 335

Asp Met Arg Leu Ile Glu Ala Val Tyr Glu Ala Gly Glu Ser Gly Arg
 340 345 350

Val Val Thr Leu Asp
 355

<210> SEQ ID NO 13

<211> LENGTH: 526

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas stutzeri

<400> SEQUENCE: 13

Met Ala Ser Val His Ser Ile Thr Tyr Glu Leu Leu Arg Arg Gln Gly
 1 5 10 15

Ile Asp Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
 20 25 30

Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Ala Leu Gln Glu Ala
 35 40 45

Cys Val Val Gly Ile Ala Asp Gly Tyr Ala Gln Ala Ser Arg Lys Pro
 50 55 60

Ala Phe Ile Asn Leu His Ser Ala Ala Gly Thr Gly Asn Ala Met Gly
 65 70 75 80

Ala Met Ser Asn Ala Trp Asn Cys His Ser Pro Leu Ile Val Thr Ala
 85 90 95

Gly Gln Gln Asn Arg Ala Met Ile Gly Val Glu Ala Leu Leu Thr Asn
 100 105 110

Val Asp Ala Ala Ser Leu Pro Arg Pro Leu Val Lys Trp Ser Tyr Glu
 115 120 125

Pro Ala Ser Ala Ala Glu Val Pro His Ala Met Ser Arg Ala Ile His
 130 135 140

Met Ala Ser Met Ala Pro Arg Gly Pro Val Tyr Leu Ser Val Pro Tyr
 145 150 155 160

Asp Asp Trp Asp Lys Glu Ala Asp Pro Gln Ser His His Leu Tyr Asp
 165 170 175

Arg Ser Val Asn Ser Ala Val Arg Leu Asn Asp Gln Asp Leu Glu Val
 180 185 190

Leu Val Glu Ala Leu Asn Ser Ala Ser Asn Pro Ala Ile Val Leu Gly
 195 200 205

Pro Asp Val Asp Ser Ala Asn Ala Asn Ala Asp Cys Val Thr Leu Ala
 210 215 220

Glu Arg Leu Lys Ala Pro Val Trp Val Ala Pro Ser Ala Pro Arg Cys
 225 230 235 240

Pro Phe Pro Thr Arg His Pro Cys Phe Arg Gly Leu Met Pro Ala Gly
 245 250 255

Ile Ala Ala Ile Ser Gln Leu Leu Glu Gly His Asp Val Val Leu Val
 260 265 270

Ile Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Asp Pro Gly Gln Tyr
 275 280 285

Leu Lys Pro Gly Thr Arg Leu Ile Ser Ile Thr Cys Asp Pro Leu Glu
 290 295 300

Ala Ala Arg Ala Pro Met Gly Asp Ala Ile Val Ala Asp Ile Gly Thr
 305 310 315 320

Met Thr Ala Ala Leu Ala Ser Arg Ile Gly Glu Ser Glu Arg Gln Leu

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325	330	335
Pro Ala Val Leu Pro Ser Pro Glu Arg Val Asn Gln Asp Ala Gly Arg		
340	345	350
Leu Arg Pro Glu Thr Val Phe Asp Thr Leu Asn Glu Met Ala Pro Glu		
355	360	365
Asp Ala Ile Tyr Leu Asn Glu Ser Thr Ser Thr Ala Gln Met Trp		
370	375	380
Gln Arg Leu Asn Met Arg Asn Pro Gly Ser Tyr Tyr Phe Cys Ala Ala		
385	390	395
Gly Gly Leu Gly Phe Ala Leu Pro Ala Ala Ile Gly Val Gln Leu Ala		
405	410	415
Glu Pro Asp Arg Gln Val Ile Ala Val Ile Gly Asp Gly Ser Ala Asn		
420	425	430
Tyr Ser Ile Ser Ala Leu Trp Thr Ala Ala His Tyr Asn Ile Pro Ala		
435	440	445
Ile Phe Leu Ile Met Asn Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe		
450	455	460
Ala Gly Val Leu Glu Ala Glu Asn Val Pro Gly Leu Asp Val Pro Gly		
465	470	475
Ile Asp Phe Cys Ala Ile Ala Lys Gly Tyr Gly Ile Pro Ala Leu Lys		
485	490	495
Ala Asp Asn Leu Glu Gln Leu Lys Gly Ser Ile His Glu Ala Leu Ser		
500	505	510
Ala Lys Gly Pro Val Leu Ile Glu Val Ser Thr Val Ser Leu		
515	520	525

<210> SEQ_ID NO 14

<211> LENGTH: 527

<212> TYPE: PRT

<213> ORGANISM: Agrobacterium radiobacter

<400> SEQUENCE: 14

Met Lys Thr Val Arg Glu Ala Thr Tyr Glu Leu Leu Arg Ser Val Gly		
1	5	10
Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu		
20	25	30
Asn Gly Phe Pro Ala Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly		
35	40	45
Val Val Val Gly Met Ala Asp Gly Tyr Ala Gln Ala Thr Gly Asn Ala		
50	55	60
Ser Leu Val Asn Leu His Ser Ala Ala Gly Thr Gly Asn Gly Met Gly		
65	70	75
80		
Ala Leu Ala Asn Ala Trp Asn Ser His Thr Pro Ile Ile Val Thr Ala		
85	90	95
Gly Gln Gln Thr Arg Ala Met Ile Gly Ala Glu Pro Leu Leu Ala Asn		
100	105	110
Val Asp Ala Ala Met Leu Pro Arg Pro Leu Val Lys Trp Ser Tyr Glu		
115	120	125
Pro Ala Ser Ala Ser Glu Val Pro His Ala Phe Ser Arg Ala Tyr His		
130	135	140
Ile Ala Glu Leu Pro Ala Lys Gly Pro Val Tyr Leu Ser Ile Pro Tyr		
145	150	155
160		
Asn Asp Trp Glu Gln Pro Ala Gly Pro Phe Ser Asp Ala Val Asn Met		
165	170	175

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Arg Lys Val Glu Ala Ala Gly Met Pro Asp Glu His Arg Leu Ala Ala
180 185 190

Leu Leu Asp Arg Ile Ala Ser Ala Arg Asn Pro Val Ile Val Leu Gly
195 200 205

Pro Asp Val Asp Ala Ala Arg Ala Asn Ser Tyr Ala Val Thr Leu Ala
210 215 220

Glu Lys Ile Ala Ala Pro Val Trp Val Ala Pro Ser Ala Pro Arg Cys
225 230 235 240

Pro Phe Pro Thr Thr His Gln Asn Phe Arg Gly Leu Leu Pro Ala Gly
245 250 255

Ile Ala Ser Ile Ser Arg Leu Leu Ser Gly His Asp Leu Ile Leu Val
260 265 270

Phe Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Asp Pro Gly Ala Trp
275 280 285

Leu Pro Glu Gly Ala Ser Leu Ile Ser Val Thr Cys Asp Ala Leu Glu
290 295 300

Ala Ala Arg Ala Pro Met Gly Asp Ala Ile Val Gly Asp Val Gly Gly
305 310 315 320

Val Leu Lys Arg Leu Cys Glu Arg Val Val Ala Gly Ala Arg Ala Asp
325 330 335

Leu Glu Ala Leu Pro Arg Pro Glu Arg Ala Pro Ala Ser Ser Gly Ala
340 345 350

Leu Leu Pro Glu Ala Val Phe Asp Ile Leu Asp Asp Leu Ala Pro Glu
355 360 365

Asn Ala Ile Tyr Leu Asn Glu Ser Thr Ser Thr Ala Ala Leu Trp
370 375 380

Glu Arg Leu Arg Met Arg Gln Pro Gly Ser Tyr Tyr Phe Ala Ala Ala
385 390 395 400

Gly Gly Leu Gly Phe Ala Met Pro Ala Ser Val Gly Val Gln Leu Ala
405 410 415

Glu Pro Glu Arg Arg Val Ile Ala Ile Ile Gly Asp Gly Ser Ala Asn
420 425 430

Tyr Gly Ile Gln Ala Leu Trp Thr Ala Ala Gln Tyr Lys Ile Pro Thr
435 440 445

Ile Phe Ile Ile Met Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
450 455 460

Ala Gly Val Leu Lys Val Glu Asn Val Pro Gly Leu Asp Val Pro Asp
465 470 475 480

Ile Asp Phe Gln Ala Leu Ala Thr Gly Tyr Gly Val Lys Ala His Arg
485 490 495

Ala Arg Asn Ala Glu Glu Phe Lys His Ala Leu Thr Glu Ala Leu Ser
500 505 510

Ser Asp Thr Pro Ile Leu Ile Glu Val Leu Thr Lys His Gly Gly
515 520 525

<210> SEQ ID NO 15

<211> LENGTH: 549

<212> TYPE: PRT

<213> ORGANISM: *Pseudomonas aeruginosa*

<400> SEQUENCE: 15

Met Ile Asp Tyr Arg Ala Ala Ala Thr Val Ala Gln Ile Gln Glu Thr
1 5 10 15

Thr Leu Lys Ala Cys Met Lys Thr Val His Ser Ala Ser Tyr Glu Ile
20 25 30

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Leu Arg Arg His Gly Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn
 35 40 45
 Glu Leu Pro Phe Leu Arg Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu
 50 55 60
 Gly Leu His Glu Gly Ala Val Val Gly Met Ala Asp Gly Phe Ala Leu
 65 70 75 80
 Ala Ser Gly Arg Pro Ala Phe Val Asn Leu His Ala Ala Gly Thr
 85 90 95
 Gly Asn Gly Met Gly Ala Leu Thr Asn Ala Trp Tyr Ser His Ser Pro
 100 105 110
 Leu Val Ile Ser Ala Gly Gln Gln Val Arg Ser Met Ile Gly Val Glu
 115 120 125
 Ala Met Leu Ala Asn Val Glu Ala Gly Gln Leu Pro Lys Pro Leu Val
 130 135 140
 Lys Trp Ser His Glu Pro Ala Cys Ala Gln Asp Val Pro Arg Ala Leu
 145 150 155 160
 Ser Gln Ala Ile Gln Ile Ala Ser Leu Pro Pro Arg Ala Pro Val Tyr
 165 170 175
 Leu Ser Ile Pro Tyr Asp Asp Trp Ala Gln Pro Ala Pro Ala Gly Val
 180 185 190
 Glu His Leu Ala Ala Arg Gln Val Ser Gly Ala Ala Leu Pro Ala Pro
 195 200 205
 Ala Leu Leu Ala Glu Leu Gly Glu Arg Leu Ser Arg Ser Arg Asn Pro
 210 215 220
 Val Leu Val Leu Gly Pro Asp Val Asp Gly Ala Asn Ala Asn Gly Leu
 225 230 235 240
 Ala Val Gln Leu Ala Glu Lys Leu Arg Met Pro Ala Trp Val Ala Pro
 245 250 255
 Ser Ala Ser Arg Cys Pro Phe Pro Thr Arg His Pro Cys Phe Arg Gly
 260 265 270
 Val Leu Pro Ala Ala Ile Ala Gly Ile Ser Arg Leu Leu Asp Gly His
 275 280 285
 Asp Leu Ile Leu Val Val Gly Ala Pro Val Phe Arg Tyr His Gln Phe
 290 295 300
 Ala Pro Gly Asp Tyr Leu Pro Ala Gly Ala Glu Leu Val Gln Ile Thr
 305 310 315 320
 Cys Asp Pro Gly Glu Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val
 325 330 335
 Gly Asp Ile Gly Leu Ser Leu Glu Ala Leu Leu Glu Gln Val Arg Pro
 340 345 350
 Ser Ala Arg Pro Leu Pro Glu Ala Leu Pro Arg Pro Pro Ala Leu Ala
 355 360 365
 Glu Glu Gly Pro Leu Arg Pro Glu Thr Val Phe Asp Val Ile Asp
 370 375 380
 Ala Leu Ala Pro Arg Asp Ala Ile Phe Val Lys Glu Ser Thr Ser Thr
 385 390 395 400
 Val Thr Ala Phe Trp Gln Arg Val Glu Met Arg Glu Pro Gly Ser Tyr
 405 410 415
 Phe Phe Pro Ala Ala Gly Leu Gly Phe Gly Leu Pro Ala Ala Val
 420 425 430
 Gly Ala Gln Leu Ala Gln Pro Arg Arg Gln Val Ile Gly Ile Ile Gly
 435 440 445

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Asp Gly Ser Ala Asn Tyr Gly Ile Thr Ala Leu Trp Ser Ala Ala Gln
450 455 460

Tyr Arg Val Pro Ala Val Phe Ile Ile Leu Lys Asn Gly Thr Tyr Gly
465 470 475 480

Ala Leu Arg Trp Phe Ala Gly Val Leu Glu Val Pro Asp Ala Pro Gly
485 490 495

Leu Asp Val Pro Gly Leu Asp Phe Cys Ala Ile Ala Arg Gly Tyr Gly
500 505 510

Val Glu Ala Leu His Ala Ala Thr Arg Glu Glu Leu Glu Ser Ala Leu
515 520 525

Lys Gln Ala Leu Ala Ala Asp Arg Pro Val Leu Ile Glu Val Pro Thr
530 535 540

Gln Thr Ile Glu Pro
545

<210> SEQ ID NO 16

<211> LENGTH: 528

<212> TYPE: PRT

<213> ORGANISM: *Pseudomonas aeruginosa*

<400> SEQUENCE: 16

Met Lys Thr Val His Ser Ala Ser Tyr Glu Ile Leu Arg Arg His Gly
1 5 10 15

Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
20 25 30

Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly
35 40 45

Ala Val Val Gly Met Ala Asp Gly Phe Ala Leu Ala Ser Gly Arg Pro
50 55 60

Ala Phe Val Asn Leu His Ala Ala Gly Thr Gly Asn Gly Met Gly
65 70 75 80

Ala Leu Thr Asn Ala Trp Tyr Ser His Ser Pro Leu Val Ile Thr Ala
85 90 95

Gly Gln Gln Val Arg Ser Met Ile Gly Val Glu Ala Met Leu Ala Asn
100 105 110

Val Asp Ala Gly Gln Leu Pro Lys Pro Leu Val Lys Trp Ser His Glu
115 120 125

Pro Ala Cys Ala Gln Asp Val Pro Arg Ala Leu Ser Gln Ala Ile Gln
130 135 140

Thr Ala Ser Leu Pro Pro Arg Ala Pro Val Tyr Leu Ser Ile Pro Tyr
145 150 155 160

Asp Asp Trp Ala Gln Pro Ala Pro Ala Gly Val Glu His Leu Ala Ala
165 170 175

Arg Gln Val Ser Gly Ala Ala Leu Pro Ala Pro Ala Leu Ala Glu
180 185 190

Leu Gly Glu Arg Leu Ser Arg Ser Arg Asn Pro Val Leu Val Leu Gly
195 200 205

Pro Asp Val Asp Gly Ala Asn Ala Asn Gly Leu Ala Val Glu Leu Ala
210 215 220

Glu Lys Leu Arg Met Pro Ala Trp Val Ala Pro Ser Ala Ser Arg Cys
225 230 235 240

Pro Phe Pro Thr Arg His Ala Cys Phe Arg Gly Val Leu Pro Ala Ala
245 250 255

Ile Ala Gly Ile Ser Arg Leu Leu Asp Gly His Asp Leu Ile Leu Val
260 265 270

Val Gly Ala Pro Val Phe Arg Tyr His Gln Phe Ala Pro Gly Asp Tyr
 275 280 285
 Leu Pro Ala Gly Ala Glu Leu Val Gln Val Thr Cys Asp Pro Gly Glu
 290 295 300
 Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val Gly Asp Ile Ala Leu
 305 310 315 320
 Thr Leu Glu Ala Leu Leu Glu Gln Val Arg Pro Ser Ala Arg Pro Leu
 325 330 335
 Pro Glu Ala Leu Pro Arg Pro Pro Ala Leu Ala Glu Glu Gly Pro
 340 345 350
 Leu Arg Pro Glu Thr Val Phe Asp Val Ile Asp Ala Leu Ala Pro Arg
 355 360 365
 Asp Ala Ile Phe Val Lys Glu Ser Thr Ser Thr Val Thr Ala Phe Trp
 370 375 380
 Gln Arg Val Glu Met Arg Glu Pro Gly Ser Tyr Phe Phe Pro Ala Ala
 385 390 395 400
 Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Ala Gln Leu Ala
 405 410 415
 Gln Pro Arg Arg Gln Val Ile Gly Ile Ile Gly Asp Gly Ser Ala Asn
 420 425 430
 Tyr Gly Ile Thr Ala Leu Trp Ser Ala Ala Gln Tyr Arg Val Pro Ala
 435 440 445
 Val Phe Ile Ile Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
 450 455 460
 Ala Gly Val Leu Glu Val Pro Asp Ala Pro Gly Leu Asp Val Pro Gly
 465 470 475 480
 Leu Asp Phe Cys Ala Ile Ala Arg Gly Tyr Gly Val Glu Ala Leu His
 485 490 495
 Ala Ala Thr Arg Glu Glu Leu Glu Gly Ala Leu Lys His Ala Leu Ala
 500 505 510
 Ala Asp Arg Pro Val Leu Ile Glu Val Pro Thr Gln Thr Ile Glu Pro
 515 520 525

<210> SEQ ID NO 17
 <211> LENGTH: 528
 <212> TYPE: PRT
 <213> ORGANISM: *Pseudomonas aeruginosa*
 <400> SEQUENCE: 17

Met Lys Thr Val His Ser Ala Ser Tyr Glu Ile Leu Arg Arg His Gly
 1 5 10 15
 Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
 20 25 30
 Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly
 35 40 45
 Ala Val Val Gly Met Ala Asp Gly Phe Ala Leu Ala Ser Gly Arg Pro
 50 55 60
 Ala Phe Val Asn Leu His Ala Ala Ala Gly Thr Gly Asn Gly Met Gly
 65 70 75 80
 Ala Leu Thr Asn Ala Trp Tyr Ser His Ser Pro Leu Val Ile Thr Ala
 85 90 95
 Gly Gln Gln Val Arg Ser Met Ile Gly Val Glu Ala Met Leu Ala Asn
 100 105 110
 Val Asp Ala Gly Gln Leu Pro Lys Pro Leu Val Lys Trp Ser His Glu

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115	120	125
Pro Ala Cys Ala Gln Asp Val Pro Arg Ala Leu Ser Gln Ala Ile Gln		
130	135	140
Thr Ala Ser Leu Pro Pro Arg Ala Pro Val Tyr Leu Ser Ile Pro Tyr		
145	150	155
Asp Asp Trp Ala Gln Pro Ala Pro Ala Gly Val Glu His Leu Ala Ala		
165	170	175
Arg Gln Val Ser Gly Ala Ala Leu Pro Ala Pro Ala Leu Leu Ala Glu		
180	185	190
Leu Gly Glu Arg Leu Ser Arg Ser Arg Asn Pro Val Leu Val Leu Gly		
195	200	205
Pro Asp Val Asp Gly Ala Asn Ala Asn Gly Leu Ala Val Gln Leu Ala		
210	215	220
Glu Lys Leu Arg Met Pro Ala Trp Val Ala Pro Ser Ala Ser Arg Cys		
225	230	235
Pro Phe Pro Thr Arg His Ala Cys Phe Arg Gly Val Leu Pro Ala Ala		
245	250	255
Ile Ala Gly Ile Ser Arg Leu Leu Asp Gly His Asp Leu Ile Leu Val		
260	265	270
Val Gly Ala Pro Val Phe Arg Tyr His Gln Phe Ala Pro Gly Asp Tyr		
275	280	285
Leu Pro Ala Gly Ala Glu Leu Val Gln Val Thr Cys Asp Pro Gly Glu		
290	295	300
Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val Gly Asp Ile Ala Leu		
305	310	315
Thr Leu Glu Ala Leu Leu Glu Gln Val Arg Pro Ser Ala Arg Pro Leu		
325	330	335
Pro Glu Ala Leu Pro Arg Pro Pro Ala Leu Ala Glu Glu Gly Pro		
340	345	350
Leu Arg Pro Glu Thr Val Phe Asp Val Ile Asp Ala Leu Ala Pro Arg		
355	360	365
Asp Ala Ile Phe Val Lys Glu Ser Thr Ser Thr Val Thr Ala Phe Trp		
370	375	380
Gln Arg Val Glu Met Arg Glu Pro Gly Ser Tyr Phe Phe Pro Ala Ala		
385	390	395
Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Ala Gln Leu Ala		
405	410	415
Gln Pro Arg Arg Gln Val Ile Gly Ile Ile Gly Asp Gly Ser Ala Asn		
420	425	430
Tyr Gly Ile Thr Ala Leu Trp Ser Ala Ala Gln Tyr Arg Val Pro Ala		
435	440	445
Val Phe Ile Ile Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe		
450	455	460
Ala Gly Val Leu Glu Val Pro Asp Ala Pro Gly Leu Asp Val Pro Gly		
465	470	475
Leu Asp Phe Cys Ala Ile Ala Arg Gly Tyr Gly Val Glu Ala Leu His		
485	490	495
Ala Ala Thr Arg Glu Glu Leu Glu Ser Ala Leu Lys His Ala Leu Ala		
500	505	510
Ala Asp Arg Pro Val Leu Ile Glu Val Pro Thr Gln Thr Ile Glu Pro		
515	520	525

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<211> LENGTH: 528
 <212> TYPE: PRT
 <213> ORGANISM: Pseudomonas aeruginosa
 <400> SEQUENCE: 18

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Met Lys Thr Val His Ser Ala Ser Tyr Glu Ile Leu Arg Arg His Gly
1           5          10          15

Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
20          25          30

Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly
35          40          45

Ala Val Val Gly Met Ala Asp Gly Phe Ala Leu Ala Ser Gly Arg Pro
50          55          60

Ala Phe Val Asn Leu His Ala Ala Ala Gly Thr Gly Asn Gly Met Gly
65          70          75          80

Ala Leu Thr Asn Ala Trp Tyr Ser His Ser Pro Leu Val Ile Thr Ala
85          90          95

Gly Gln Gln Val Arg Ser Met Ile Gly Val Glu Ala Met Leu Ala Asn
100         105         110

Val Asp Ala Gly Gln Leu Pro Lys Pro Leu Val Lys Trp Ser His Glu
115         120         125

Pro Ala Cys Ala Gln Asp Val Pro Arg Ala Leu Ser Gln Ala Ile Gln
130         135         140

Thr Ala Ser Leu Pro Pro Arg Ala Pro Val Tyr Leu Ser Ile Pro Tyr
145         150         155         160

Asp Asp Trp Ala Gln Pro Ala Pro Val Gly Val Glu His Leu Ala Ala
165         170         175

Arg Gln Val Ser Gly Ala Ala Leu Pro Ala Pro Ala Leu Ala Glu
180         185         190

Leu Gly Glu Arg Leu Ser Arg Ser Arg Asn Pro Val Leu Val Leu Gly
195         200         205

Pro Asp Val Asp Gly Ala Asn Ala Asn Gly Leu Ala Val Glu Leu Ala
210         215         220

Glu Lys Leu Arg Met Pro Ala Trp Val Ala Pro Ser Ala Ser Arg Cys
225         230         235         240

Pro Phe Pro Thr Arg His Ala Cys Phe Arg Gly Val Leu Pro Ala Ala
245         250         255

Ile Ala Gly Ile Ser Arg Leu Leu Asp Gly His Asp Leu Ile Leu Val
260         265         270

Val Gly Ala Pro Val Phe Arg Tyr His Gln Phe Ala Pro Gly Asp Tyr
275         280         285

Leu Pro Ala Gly Ala Glu Leu Val Gln Val Thr Cys Asp Pro Gly Glu
290         295         300

Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val Gly Asp Ile Ala Leu
305         310         315         320

Thr Leu Glu Ala Leu Leu Glu Gln Val Arg Pro Ser Ala Arg Pro Leu
325         330         335

Pro Glu Ala Leu Pro Arg Pro Pro Ala Leu Ala Glu Glu Gly Pro
340         345         350

Leu Arg Pro Glu Thr Val Phe Asp Val Ile Asp Ala Leu Ala Pro Arg
355         360         365

Asp Ala Ile Phe Val Lys Glu Ser Thr Ser Thr Val Thr Ala Phe Trp
370         375         380

Gln Arg Val Glu Met Arg Glu Pro Gly Ser Tyr Phe Phe Pro Ala Ala

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385	390	395	400
Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Ala Gln Leu Ala			
405	410	415	
Gln Pro Arg Arg Gln Val Ile Gly Ile Ile Gly Asp Gly Ser Ala Asn			
420	425	430	
Tyr Gly Ile Thr Ala Leu Trp Ser Ala Ala Gln Tyr Arg Val Pro Ala			
435	440	445	
Val Phe Ile Ile Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe			
450	455	460	
Ala Gly Val Leu Glu Val Pro Asp Ala Pro Gly Leu Asp Val Pro Gly			
465	470	475	480
Leu Asp Phe Cys Ala Ile Ala Arg Gly Tyr Gly Val Glu Ala Leu His			
485	490	495	
Ala Ala Thr Arg Glu Glu Leu Glu Ser Ala Leu Lys His Ala Leu Ala			
500	505	510	
Ala Asp Arg Pro Val Leu Ile Glu Val Pro Thr Gln Thr Ile Glu Pro			
515	520	525	

<210> SEQ_ID NO 19

<211> LENGTH: 528

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 19

Met Lys Thr Val His Ser Ala Ser Tyr Glu Ile Leu Arg Arg His Gly			
1	5	10	15
Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu			
20	25	30	
Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly			
35	40	45	
Ala Val Val Gly Met Ala Asp Gly Phe Ala Leu Ala Ser Gly Arg Pro			
50	55	60	
Ala Phe Val Asn Leu His Ala Ala Gly Thr Gly Asn Gly Met Gly			
65	70	75	80
Ala Leu Thr Asn Ala Trp Tyr Ser His Ser Pro Leu Val Ile Thr Ala			
85	90	95	
Gly Gln Gln Val Arg Ser Met Ile Gly Val Glu Ala Met Leu Ala Asn			
100	105	110	
Val Asp Ala Gly Gln Leu Pro Lys Pro Leu Val Lys Trp Ser His Glu			
115	120	125	
Pro Ala Cys Ala Gln Asp Val Pro Arg Ala Leu Ser Gln Ala Ile Gln			
130	135	140	
Thr Ala Ser Leu Pro Pro Arg Ala Pro Val Tyr Leu Ser Ile Pro Tyr			
145	150	155	160
Asp Asp Trp Ala Gln Pro Ala Pro Ala Gly Val Glu His Leu Ala Ala			
165	170	175	
Arg Gln Val Ser Gly Ala Ala Leu Pro Ala Pro Ala Leu Ala Glu			
180	185	190	
Leu Gly Glu Arg Leu Ser Arg Ser Arg Asn Pro Val Leu Val Leu Gly			
195	200	205	
Pro Asp Val Asp Gly Ala Asn Ala Asn Gly Leu Ala Val Glu Leu Ala			
210	215	220	
Glu Lys Leu Arg Met Pro Ala Trp Val Ala Pro Ser Ala Ser Arg Cys			
225	230	235	240

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Pro Phe Pro Thr Arg His Ala Cys Phe Arg Gly Val Leu Pro Ala Ala
245 250 255

Ile Ala Gly Ile Ser Arg Leu Leu Asp Gly His Asp Leu Ile Leu Val
260 265 270

Val Gly Ala Pro Val Phe Arg Tyr His Gln Phe Ala Pro Gly Asp Tyr
275 280 285

Leu Pro Ala Gly Ala Glu Leu Val Gln Val Thr Cys Asp Pro Gly Glu
290 295 300

Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val Gly Asp Ile Ala Leu
305 310 315 320

Thr Leu Glu Ala Leu Leu Glu Gln Val Arg Pro Ser Ala Arg Pro Leu
325 330 335

Pro Glu Ala Leu Pro Arg Pro Ala Leu Ala Glu Glu Gly Gly Pro
340 345 350

Leu Arg Pro Glu Thr Val Phe Asp Val Ile Asp Ala Leu Ala Pro Arg
355 360 365

Asp Ala Ile Phe Val Lys Glu Ser Thr Ser Thr Val Thr Ala Phe Trp
370 375 380

Gln Arg Val Glu Met Arg Glu Pro Gly Ser Tyr Phe Phe Pro Ala Ala
385 390 395 400

Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Ala Gln Leu Ala
405 410 415

Gln Pro Arg Arg Gln Val Ile Gly Ile Gly Asp Gly Ser Ala Asn
420 425 430

Tyr Gly Ile Thr Ala Leu Trp Ser Ala Ala Gln Tyr Arg Val Pro Ala
435 440 445

Val Phe Ile Ile Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
450 455 460

Ala Gly Val Leu Glu Val Pro Asp Ala Pro Gly Leu Asp Val Pro Gly
465 470 475 480

Leu Asp Phe Cys Ala Ile Ala Arg Gly Tyr Gly Val Glu Ala Leu His
485 490 495

Ala Ala Thr Arg Glu Glu Leu Glu Ser Ala Leu Lys His Ala Leu Ala
500 505 510

Ala Asp Arg Pro Val Leu Ile Glu Val Pro Thr Gln Thr Ile Glu Pro
515 520 525

<210> SEQ ID NO 20

<211> LENGTH: 528

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 20

Met Lys Thr Val His Ser Ala Ser Tyr Glu Ile Leu Arg Arg His Gly
1 5 10 15Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
20 25 30Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly
35 40 45Ala Val Val Gly Met Ala Asp Gly Phe Ala Leu Ala Ser Gly Arg Pro
50 55 60Ala Phe Val Asn Leu His Ala Ala Ala Gly Thr Gly Asn Gly Met Gly
65 70 75 80Ala Leu Thr Asn Ala Trp Tyr Ser His Ser Pro Leu Val Ile Thr Ala
85 90 95

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Gly Gln Gln Val Arg Ser Met Ile Gly Val Glu Ala Met Leu Ala Asn
100 105 110

Val Asp Ala Gly Gln Leu Pro Lys Pro Leu Val Lys Trp Ser His Glu
115 120 125

Pro Ala Cys Ala Gln Asp Val Pro Arg Ala Leu Ser Gln Ala Ile Gln
130 135 140

Thr Ala Ser Leu Pro Pro Arg Ala Pro Val Tyr Leu Ser Ile Pro Tyr
145 150 155 160

Asp Asp Trp Ala Gln Pro Ala Pro Val Gly Val Glu His Leu Ala Ala
165 170 175

Arg Gln Val Ser Gly Ala Ala Leu Pro Ala Pro Ala Leu Ala Glu
180 185 190

Leu Gly Glu Arg Leu Ser Arg Ser Arg Asn Pro Val Leu Val Leu Gly
195 200 205

Pro Asp Val Asp Gly Ala Asn Ala Asn Gly Leu Ala Val Glu Leu Ala
210 215 220

Glu Lys Leu Arg Met Pro Ala Trp Val Ala Pro Ser Ala Ser Arg Cys
225 230 235 240

Pro Phe Pro Thr Arg His Ala Cys Phe Arg Gly Val Leu Pro Ala Ala
245 250 255

Ile Ala Gly Ile Ser Arg Leu Leu Asp Gly His Asp Leu Ile Leu Val
260 265 270

Val Gly Ala Pro Val Phe Arg Tyr His Gln Phe Ala Pro Gly Asp Tyr
275 280 285

Leu Pro Ala Gly Ala Glu Leu Val Gln Val Thr Cys Asp Pro Gly Glu
290 295 300

Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val Gly Asp Ile Ala Leu
305 310 315 320

Thr Leu Glu Ala Leu Leu Glu Gln Val Arg Pro Ser Ala Arg Pro Leu
325 330 335

Pro Glu Ala Leu Pro Arg Pro Pro Ala Leu Ala Glu Glu Gly Pro
340 345 350

Leu Arg Pro Glu Thr Val Phe Asp Val Ile Asp Ala Leu Ala Pro Arg
355 360 365

Asp Ala Ile Phe Val Lys Glu Ser Thr Ser Thr Val Thr Ala Phe Trp
370 375 380

Gln Arg Val Glu Met Arg Glu Pro Gly Ser Tyr Phe Phe Pro Ala Ala
385 390 395 400

Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Ala Gln Leu Ala
405 410 415

Gln Pro Arg Arg Gln Val Ile Gly Ile Ile Gly Asp Gly Ser Ala Asn
420 425 430

Tyr Gly Ile Thr Ala Leu Trp Ser Ala Ala Gln Tyr Arg Val Pro Ala
435 440 445

Val Phe Ile Ile Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
450 455 460

Ala Gly Val Leu Glu Val Pro Asp Ala Pro Gly Leu Asp Val Pro Gly
465 470 475 480

Leu Asp Phe Cys Ala Ile Val Arg Gly Tyr Gly Val Glu Ala Leu His
485 490 495

Ala Ala Thr Arg Glu Glu Leu Glu Ser Ala Leu Lys His Ala Leu Ala
500 505 510

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Ala Asp Arg Pro Val Leu Ile Glu Val Pro Thr Gln Thr Ile Glu Pro
515 520 525

<210> SEQ ID NO 21
 <211> LENGTH: 528
 <212> TYPE: PRT
 <213> ORGANISM: *Pseudomonas putida*
 <400> SEQUENCE: 21

 Met Lys Thr Val His Gly Ala Thr Tyr Asp Ile Leu Arg Gln His Gly
 1 5 10 15

 Leu Thr Thr Ile Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
 20 25 30

 Lys Gly Phe Pro Glu Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly
 35 40 45

 Ala Val Val Gly Met Ala Asp Gly Tyr Ala Leu Ala Ser Gly Gln Pro
 50 55 60

 Thr Phe Val Asn Leu His Ala Ala Ala Gly Thr Gly Asn Gly Met Gly
 65 70 75 80

 Ala Leu Thr Asn Ala Trp Tyr Ser His Ser Pro Leu Val Ile Thr Ala
 85 90 95

 Gly Gln Gln Val Arg Ser Met Ile Gly Val Glu Ala Met Leu Ala Asn
 100 105 110

 Val Asp Ala Ala Gln Leu Pro Lys Pro Leu Val Lys Trp Ser His Glu
 115 120 125

 Pro Ala Thr Ala Gln Asp Val Pro Arg Ala Leu Ser Gln Ala Ile His
 130 135 140

 Thr Ala Asn Leu Pro Pro Arg Gly Pro Val Tyr Val Ser Ile Pro Tyr
 145 150 155 160

 Asp Asp Trp Ala Cys Glu Ala Pro Ser Gly Val Glu His Leu Ala Arg
 165 170 175

 Arg Gln Val Ser Ser Ala Gly Leu Pro Ser Pro Ala Gln Leu Gln His
 180 185 190

 Leu Cys Glu Arg Leu Ala Ala Arg Asn Pro Val Leu Val Leu Gly
 195 200 205

 Pro Asp Val Asp Gly Ser Ala Ala Asn Gly Leu Ala Val Gln Leu Ala
 210 215 220

 Glu Lys Leu Arg Met Pro Ala Trp Val Ala Pro Ser Ala Ser Arg Cys
 225 230 235 240

 Pro Phe Pro Thr Arg His Ala Cys Phe Arg Gly Val Leu Pro Ala Ala
 245 250 255

 Ile Ala Gly Ile Ser His Asn Leu Ala Gly His Asp Leu Ile Leu Val
 260 265 270

 Val Gly Ala Pro Val Phe Arg Tyr His Gln Phe Ala Pro Gly Asn Tyr
 275 280 285

 Leu Pro Ala Gly Cys Glu Leu Leu His Leu Thr Cys Asp Pro Gly Glu
 290 295 300

 Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val Gly Asp Ile Ala Leu
 305 310 315 320

 Thr Leu Glu Ala Val Leu Asp Gly Val Pro Gln Ser Val Arg Gln Met
 325 330 335

 Pro Thr Ala Leu Pro Ala Ala Glu Pro Val Ala Asp Asp Gly Gly Leu
 340 345 350

 Leu Arg Pro Glu Thr Val Phe Asp Leu Leu Asn Ala Leu Ala Pro Lys
 355 360 365

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Asp Ala Ile Tyr Val Lys Glu Ser Thr Ser Thr Val Gly Ala Phe Trp
 370 375 380

Arg Arg Val Glu Met Arg Glu Pro Gly Ser Tyr Phe Phe Pro Ala Ala
 385 390 395 400

Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Val Gln Leu Ala
 405 410 415

Ser Pro Gly Arg Gln Val Ile Gly Val Ile Gly Asp Gly Ser Ala Asn
 420 425 430

Tyr Gly Ile Thr Ala Leu Trp Thr Ala Ala Gln Tyr Asn Ile Pro Val
 435 440 445

Val Phe Ile Ile Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
 450 455 460

Ala Asp Val Leu Asp Val Asn Asp Ala Pro Gly Leu Asp Val Pro Gly
 465 470 475 480

Leu Asp Phe Cys Ala Ile Ala Arg Gly Tyr Gly Val Gln Ala Val His
 485 490 495

Ala Ala Thr Gly Ser Ala Phe Ala Gln Ala Leu Arg Glu Ala Leu Glu
 500 505 510

Ser Asp Arg Pro Val Leu Ile Glu Val Pro Thr Gln Thr Ile Glu Pro
 515 520 525

<210> SEQ ID NO 22

<211> LENGTH: 525

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas pudita

<400> SEQUENCE: 22

Met Lys Thr Val His Gly Ala Thr Tyr Asp Ile Leu Arg Gln His Gly
 1 5 10 15

Leu Thr Thr Ile Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
 20 25 30

Lys Gly Phe Pro Glu Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly
 35 40 45

Ala Val Val Gly Met Ala Asp Gly Tyr Ala Leu Ala Ser Gly Gln Pro
 50 55 60

Thr Phe Val Asn Leu His Ala Ala Ala Gly Thr Gly Asn Gly Met Gly
 65 70 75 80

Ala Leu Thr Asn Ala Trp Tyr Ser His Ser Pro Leu Val Ile Thr Ala
 85 90 95

Gly Gln Gln Val Arg Ser Met Ile Gly Val Glu Ala Met Leu Ala Asn
 100 105 110

Val Asp Ala Ala Gln Leu Pro Lys Pro Leu Val Lys Trp Ser His Glu
 115 120 125

Pro Ala Thr Ala Gln Asp Val Pro Arg Ala Leu Ser Gln Ala Ile His
 130 135 140

Thr Ala Asn Leu Pro Pro Arg Gly Pro Val Tyr Val Ser Ile Pro Tyr
 145 150 155 160

Asp Asp Trp Ala Cys Glu Ala Pro Ser Gly Val Glu His Leu Ala Arg
 165 170 175

Arg Gln Val Ser Ser Ala Gly Leu Pro Ser Pro Ala Gln Leu Gln His
 180 185 190

Leu Cys Glu Arg Leu Ala Ala Arg Asn Pro Val Leu Val Leu Gly
 195 200 205

Pro Asp Val Asp Gly Ser Ala Ala Asn Gly Leu Ala Val Gln Leu Ala

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210	215	220
Glu Lys Leu Arg Met Pro Ala Trp Val Ala Pro Ser Ala Ser Arg Cys		
225	230	235
240		
Pro Phe Pro Thr Arg His Ala Cys Phe Arg Gly Val Leu Pro Ala Ala		
245	250	255
Ile Ala Gly Ile Ser His Asn Leu Ala Gly His Asp Leu Ile Leu Val		
260	265	270
Val Gly Ala Pro Val Phe Arg Tyr His Gln Phe Ala Pro Gly Asn Tyr		
275	280	285
Leu Pro Ala Gly Cys Glu Leu Leu His Leu Thr Cys Asp Pro Gly Glu		
290	295	300
Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val Gly Asp Ile Ala Leu		
305	310	315
320		
Thr Leu Glu Ala Val Leu Asp Gly Val Pro Gln Ser Val Arg Gln Met		
325	330	335
Pro Thr Ala Leu Pro Ala Ala Glu Pro Val Ala Asp Asp Gly Gly Leu		
340	345	350
Leu Arg Pro Glu Thr Val Phe Asp Leu Leu Asn Ala Leu Ala Pro Lys		
355	360	365
Asp Ala Ile Tyr Val Lys Glu Ser Thr Ser Thr Val Gly Ala Phe Trp		
370	375	380
Arg Arg Val Glu Met Arg Glu Pro Gly Ser Tyr Phe Phe Pro Ala Ala		
385	390	395
400		
Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Val Gln Leu Ala		
405	410	415
Ser Pro Gly Arg Gln Val Ile Gly Val Ile Gly Asp Gly Ser Ala Asn		
420	425	430
Tyr Gly Ile Thr Ala Leu Trp Thr Ala Ala Gln Tyr Asn Ile Pro Val		
435	440	445
Val Phe Ile Ile Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe		
450	455	460
Ala Asp Val Leu Asp Val Asn Asp Ala Pro Gly Leu Asp Val Pro Gly		
465	470	475
480		
Leu Asp Phe Cys Ala Ile Ala Arg Gly Tyr Gly Val Gln Ala Val His		
485	490	495
Ala Ala Thr Gly Ser Ala Phe Ala Gln Ala Leu Arg Glu Ala Leu Glu		
500	505	510
Ser Asp Arg Pro Val Leu Ile Cys Ala Ala Ser Ser Arg		
515	520	525

<210> SEQ ID NO 23

<211> LENGTH: 528

<212> TYPE: PRT

<213> ORGANISM: Pseudomonas fluorescens

<400> SEQUENCE: 23

Met Lys Thr Val His Ser Ala Ser Tyr Asp Ile Leu Arg Gln Gln Gly		
1	5	10
15		

Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu		
20	25	30

Lys Gly Phe Pro Glu Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly		
35	40	45

Ala Val Val Gly Met Ala Asp Gly Phe Ala Leu Ala Ser Gly Gln Pro		
50	55	60

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Ala Phe Val Asn Leu His Ala Ala Ala Gly Thr Gly Asn Gly Met Gly
 65 70 75 80
 Ala Leu Thr Asn Ala Trp Tyr Ser His Ser Pro Leu Val Ile Thr Ala
 85 90 95
 Gly Gln Gln Val Arg Ser Met Ile Gly Val Glu Ala Met Leu Ala Asn
 100 105 110
 Val Asp Ala Pro Gln Leu Pro Lys Pro Leu Val Lys Trp Ser Ala Glu
 115 120 125
 Pro Ala Cys Ala Glu Asp Val Pro Arg Ala Leu Ser Gln Ala Ile His
 130 135 140
 Met Ala Asn Gln Ala Pro Lys Gly Pro Val Tyr Leu Ser Ile Pro Tyr
 145 150 155 160
 Asp Asp Trp Ala Arg Pro Ala Pro Ala Gly Val Glu His Leu Ala Arg
 165 170 175
 Arg Gln Val Ala Thr Ala Gly Leu Pro Ser Ala Ala Gln Leu Arg Ser
 180 185 190
 Leu Val Gln Arg Leu Ala Ala Arg Asn Pro Val Leu Val Leu Gly
 195 200 205
 Pro Asp Val Asp Gly Ser Arg Ser Asn His Leu Ala Val Gln Leu Ala
 210 215 220
 Glu Lys Leu Arg Met Pro Ala Trp Val Ala Pro Ser Ala Ser Arg Cys
 225 230 235 240
 Pro Phe Pro Thr Arg His Pro Ser Phe Arg Gly Val Leu Pro Ala Ala
 245 250 255
 Ile Ala Gly Ile Ser Arg Cys Leu Ala Asp His Asp Leu Ile Leu Val
 260 265 270
 Val Gly Ala Pro Val Phe Arg Tyr His Gln Phe Ala Pro Gly Asp Tyr
 275 280 285
 Leu Pro Ala Gly Thr Glu Leu Leu His Ile Thr Cys Asp Pro Gly Glu
 290 295 300
 Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val Gly Asp Ile Val Glu
 305 310 315 320
 Thr Leu Gln Ala Leu Val Trp Ala Leu Pro Asp Cys Asp Arg Pro Gln
 325 330 335
 Pro Gln Ala Leu Pro Pro Ala Ala Pro Val Glu Glu Leu Gly Leu
 340 345 350
 Leu Arg Pro Glu Thr Val Phe Asp Val Ile Asp Glu Leu Ala Pro Lys
 355 360 365
 Asp Ala Ile Tyr Val Lys Glu Ser Thr Ser Thr Val Gly Ala Phe Trp
 370 375 380
 Gln Arg Val Glu Met Arg Glu Pro Gly Ser Tyr Tyr Phe Pro Ala Ala
 385 390 395 400
 Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Val Gln Leu Ala
 405 410 415
 Arg Pro Glu Arg Arg Val Ile Gly Val Ile Gly Asp Gly Ser Ala Asn
 420 425 430
 Tyr Gly Ile Thr Ala Leu Trp Thr Ala Ala Gln Tyr Gln Ile Pro Val
 435 440 445
 Val Phe Ile Ile Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
 450 455 460
 Ala Gly Val Leu Gln Val Ser Asp Ala Pro Gly Leu Asp Val Pro Gly
 465 470 475 480
 Leu Asp Phe Cys Ala Ile Gly Arg Gly Tyr Gly Val His Ser Val Gln

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485	490	495
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Ala Asn Thr Arg Glu Ala Phe Ala Gln Ala Leu Ser Glu Ala Leu Ala
500 505 510

Gly Asp Arg Pro Val Leu Ile Glu Val Pro Thr Leu Thr Ile Glu Pro
515 520 525

<210> SEQ ID NO 24

<211> LENGTH: 529

<212> TYPE: PRT

<213> ORGANISM: Klebsiella sp.

<400> SEQUENCE: 24

Met Lys Thr Ile His Ser Ala Ala Tyr Ala Leu Leu Arg Arg His Gly
1 5 10 15

Met Thr Thr Ile Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
20 25 30

Lys Ser Phe Pro Glu Asp Phe Gln Tyr Val Leu Gly Leu His Glu Gly
35 40 45

Ala Val Val Gly Met Ala Asp Gly Tyr Ala Leu Ala Ser Gly Lys Pro
50 55 60

Ala Phe Val Asn Leu His Ala Ala Ala Gly Thr Gly Asn Gly Met Gly
65 70 75 80

Ala Leu Thr Asn Ser Trp Tyr Ser His Ser Pro Leu Val Ile Thr Ala
85 90 95

Gly Gln Gln Val Arg Pro Met Ile Gly Val Glu Ala Met Leu Ala Asn
100 105 110

Val Asp Ala Thr Gln Leu Pro Lys Pro Leu Val Lys Trp Ser Tyr Glu
115 120 125

Pro Ala Asn Ala Gln Asp Val Pro Arg Ala Leu Ser Gln Ala Ile His
130 135 140

Tyr Ala Asn Thr Thr Pro Lys Ala Pro Val Tyr Leu Ser Ile Pro Tyr
145 150 155 160

Asp Asp Trp Asp Gln Pro Ser Gly Pro Gly Val Glu His Leu Ile Glu
165 170 175

Arg Asp Val Gln Thr Ala Gly Thr Pro Asp Ala Arg Gln Leu Gln Val
180 185 190

Leu Val Gln Gln Val Gln Asp Ala Arg Asn Pro Val Leu Val Leu Gly
195 200 205

Pro Asp Val Asp Ala Thr Leu Ser Asn Asp His Ala Val Ala Leu Ala
210 215 220

Asp Lys Leu Arg Met Pro Val Trp Ile Ala Pro Ser Ala Ser Arg Cys
225 230 235 240

Pro Phe Pro Thr Arg His Pro Ser Phe Arg Gly Val Leu Pro Ala Ala
245 250 255

Ile Ala Gly Ile Ser Lys Thr Leu Gln Gly His Asp Leu Ile Ile Val
260 265 270

Val Gly Ala Pro Val Phe Arg Tyr His Gln Phe Ala Pro Gly Asp Tyr
275 280 285

Leu Pro Val Gly Ala Gln Leu Leu His Ile Thr Ser Asp Pro Leu Glu
290 295 300

Ala Thr Arg Ala Pro Met Gly His Ala Leu Val Gly Asp Ile Arg Glu
305 310 315 320

Thr Leu Arg Val Leu Ala Glu Glu Val Val Gln Gln Ser Arg Pro Tyr
325 330 335

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Pro Glu Ala Leu Ala Ala Pro Glu Cys Val Thr Asp Glu Pro His His
340 345 350

Leu His Pro Glu Thr Leu Phe Asp Val Leu Asp Ala Val Ala Pro His
355 360 365

Asp Ala Ile Tyr Val Lys Glu Ser Thr Ser Thr Thr Ala Phe Trp
370 375 380

Gln Arg Met Asn Leu Arg His Pro Gly Ser Tyr Tyr Phe Pro Ala Ala
385 390 395 400

Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Val Gln Leu Ala
405 410 415

Gln Pro Gln Arg Arg Val Val Ala Leu Ile Gly Asp Gly Ser Ala Asn
420 425 430

Tyr Gly Ile Thr Ala Leu Trp Thr Ala Ala Gln Tyr Arg Ile Pro Val
435 440 445

Val Phe Ile Ile Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
450 455 460

Ala Gly Val Leu Lys Ala Glu Asp Ser Pro Gly Leu Asp Val Pro Gly
465 470 475 480

Leu Asp Phe Cys Ala Ile Ala Lys Gly Tyr Gly Val Lys Ala Val His
485 490 495

Thr Asp Thr Arg Asp Ser Phe Glu Ala Ala Leu Arg Thr Ala Leu Asp
500 505 510

Ala Asn Glu Pro Thr Val Ile Glu Val Pro Thr Leu Thr Ile Gln Pro
515 520 525

His

<210> SEQ_ID NO 25

<211> LENGTH: 522

<212> TYPE: PRT

<213> ORGANISM: Burkholderia xenovorans

<400> SEQUENCE: 25

Met Lys Thr Val Gln His Ala Ala Tyr Glu Ile Leu Arg Arg His Gly
1 5 10 15

Leu Thr Thr Ile Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
20 25 30

Lys His Phe Pro Ser Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly
35 40 45

Val Val Thr Gly Met Ala Asp Gly Tyr Ala Gln Ala Thr Gly Asn Pro
50 55 60

Ala Phe Val Asn Leu His Ser Ala Ala Gly Thr Gly Asn Ala Met Gly
65 70 75 80

Ala Leu Ala Asn Ala Trp Asn Ser His Thr Pro Leu Val Val Thr Ser
85 90 95

Gly Gln Gln Val Arg Ser Thr Ile Gly Met Glu Pro Leu Leu Ala Asn
100 105 110

Val Asp Ala Val Asn Leu Pro Arg Pro Leu Val Lys Trp Ser Thr Glu
115 120 125

Pro Ala Ser Ala Glu Asp Val Pro Arg Ser Phe Ala Gln Ala Ile His
130 135 140

Ile Ala Arg Thr Pro Ala Thr Gly Pro Val Tyr Leu Ser Ile Pro Tyr
145 150 155 160

Asp Asp Trp Asp Gln Pro Ala Pro Glu Tyr Ala His Tyr Leu Ala Ala
165 170 175

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Arg Glu Val Gly Leu Pro Ser Glu Ala Ile Leu Gln Ala Leu Ala Asp
180 185 190

Arg Leu Gln Arg Ala Thr Asn Pro Val Leu Val Leu Gly Pro Asp Val
195 200 205

Asp Ala Gln His Ala Asn Glu Ser Ala Val Ala Leu Ala Glu Arg Leu
210 215 220

Lys Met Pro Ala Trp Met Ala Pro Ser Ala Pro Arg Cys Ser Phe Pro
225 230 235 240

Thr Thr His Ala Cys Phe Arg Gly Val Leu Pro Ala Gly Ile Ala Ser
245 250 255

Ile Ser Arg Leu Leu Asp Gly His Asp Leu Ile Leu Val Val Gly Ala
260 265 270

Pro Val Phe Arg Tyr His Gln Tyr Glu Pro Gly Ala Leu Leu Pro Ala
275 280 285

Gly Ala Glu Leu Val Ser Ile Thr Cys Asp Val Leu Glu Ala Ala Arg
290 295 300

Ala Pro Met Gly Asp Ala Ile Val Ala Asp Ile Ala Leu Thr Leu Glu
305 310 315 320

Ala Leu Ala Ala Arg Ala Glu Pro Ala Ala Arg Pro Met Pro Val Ala
325 330 335

Val Ala Arg Pro Ala Ala Ala Glu Thr Pro Gly Pro Leu Ala Pro
340 345 350

Glu Arg Val Phe Asp Ile Val Asp Ala Ile Ala Pro Arg Asp Ala Ile
355 360 365

Tyr Val Asn Glu Ser Thr Ser Thr Thr Asn Leu Met Trp Gln Arg Leu
370 375 380

Arg Met Thr Ser Gln Gly Ser Tyr Tyr Phe Ala Ala Ala Gly Gly Leu
385 390 395 400

Gly Phe Ala Met Pro Ala Ala Ala Gly Ile Gln Leu Ala Gln Pro Gly
405 410 415

Arg Arg Val Ile Gly Ile Ile Gly Asp Gly Ser Ala Asn Tyr Gly Ile
420 425 430

Thr Ala Leu Trp Thr Ala Ala Gln Tyr Ser Ile Pro Thr Ile Phe Ile
435 440 445

Ile Met Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe Ala Gly Val
450 455 460

Leu Gly Val Glu Asp Val Pro Gly Leu Tyr Val Pro Gly Ile Asp Phe
465 470 475 480

Cys Ala Leu Ala Arg Gly Tyr Gly Val Glu Ala Leu His Ala Asp Ser
485 490 495

Gly Ala Ser Leu Thr Val Ala Leu Glu Arg Ala Leu Ser Ser Ser Arg
500 505 510

Pro Thr Leu Ile Glu Val Glu Thr Leu Ala
515 520

<210> SEQ ID NO 26

<211> LENGTH: 528

<212> TYPE: PRT

<213> ORGANISM: Methylocella sylvestris

<400> SEQUENCE: 26

Met Thr Thr Ile Arg His Leu Thr Tyr Asp Leu Leu Arg Arg His Gly
1 5 10 15

Val Thr Thr Ile Phe Gly Asn Pro Gly Ser Asn Glu Leu Leu Phe Leu
20 25 30

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Glu Asp Phe Pro Ser Asp Phe Arg Tyr Ile Leu Ala Leu His Glu Gly
35 40 45

Ala Ala Ile Gly Met Ala Asp Gly Tyr Ala Gln Ala Thr Gly His Thr
50 55 60

Gly Phe Val Asn Leu His Ser Ala Ala Gly Thr Gly Asn Ala Met Gly
65 70 75 80

Gly Phe Ala Asn Ala Trp Asn Ala His Thr Pro Leu Val Val Thr Ala
85 90 95

Gly Gln Gln Val Arg Ala Met Met Gly Ile Glu Pro Leu Leu Thr Asn
100 105 110

Ile Asp Ala Thr Thr Leu Pro Lys Pro Leu Val Lys Trp Ser Cys Glu
115 120 125

Pro Ala Arg Ala Glu Asp Val Pro Leu Ala Ile Ser Arg Ala Leu His
130 135 140

Leu Ser Ala Leu Pro Ala Pro Gly Pro Val Tyr Leu Ser Ile Pro Tyr
145 150 155 160

Asp Asp Trp Asp Lys Pro Ala Glu Pro Glu Ser Leu Arg Leu Leu Lys
165 170 175

Arg Ala Val Ser Ala Ala Gly Ala Leu Asp Ala Gly Ala Leu Ala Ala
180 185 190

Leu Ala Ala Arg Leu Asp Arg Ser Ala Asn Pro Val Ile Val Leu Gly
195 200 205

Pro Asp Val Asp Ala Ala Arg Ala Asn Ala His Ala Val Arg Leu Ala
210 215 220

Glu Arg Leu Lys Ala Pro Val Trp Val Ala Pro Ser Ala Pro Arg Cys
225 230 235 240

Pro Phe Pro Thr Thr His Pro Asn Phe Arg Gly Leu Leu Thr Ala Ser
245 250 255

Met Ala Asp Ile Ser Arg Gln Leu Glu Gly His Asp Leu Val Leu Val
260 265 270

Ala Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Glu Pro Gly Pro Leu
275 280 285

Leu Pro Pro Gly Ala Glu Leu Ile Gln Ile Thr Cys Asp Ala Asp Glu
290 295 300

Ala Ala Arg Ala Pro Met Gly Asp Ala Val Val Gly Asp Val Gly Arg
305 310 315 320

Ile Leu Ala Ala Leu Ala Asp Lys Ile Gly Glu Ala Ala Arg Pro Ala
325 330 335

Pro Gln Pro Arg Glu Thr Pro Ala Pro Ser Ala Pro Gly Ser Val Pro
340 345 350

Leu Ala Ala Glu Arg Val Leu Asp Leu Met Asp Glu Leu Ala Pro Ser
355 360 365

Asp Ala Ile Tyr Val Asn Glu Ser Thr Ser Thr Ile Glu Ala Met Trp
370 375 380

Glu Arg Met Arg Trp Glu His Pro Gly Ser Tyr Tyr Phe Gly Ala Ala
385 390 395 400

Gly Gly Leu Gly Phe Ala Met Pro Ala Ala Val Gly Val Gln Leu Ala
405 410 415

Glu Pro Asp Arg Gln Val Ile Ala Leu Ile Gly Asp Gly Ser Ala Asn
420 425 430

Tyr Ser Val Thr Ala Leu Trp Thr Ala Ala Gln His Ser Val Pro Val
435 440 445

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Val Phe Val Ile Leu Arg Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
450 455 460

Ala Arg Ala Leu Lys Ala Glu His Val Pro Ala Leu Asp Val Pro Asp
465 470 475 480

Ile Asp Phe Val Ala Ile Ala Thr Gly Tyr Gly Val Glu Ala Val Arg
485 490 495

Val Asp Thr Asp Glu Ala Phe Ala Ser Ala Phe Ala Arg Ala Leu Lys
500 505 510

Ala Gly Lys Pro Ser Leu Ile Glu Val Ala Thr Ala Trp Pro Ala Thr
515 520 525

<210> SEQ ID NO 27

<211> LENGTH: 529

<212> TYPE: PRT

<213> ORGANISM: Arthrobacter sp.

<400> SEQUENCE: 27

Met Thr Thr Val His Ala Ala Ala Tyr Glu Leu Leu Arg Ser Asn Arg
1 5 10 15

Leu Thr Thr Ile Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
20 25 30

Asp Ala Met Pro Ala Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly
35 40 45

Val Val Val Gly Met Ala Asp Gly Phe Ala Gln Ala Ser Gly Gln Ala
50 55 60

Ala Phe Val Asn Leu His Ala Ala Ser Gly Thr Gly Asn Ala Met Gly
65 70 75 80

Ala Leu Thr Asn Ala Trp Tyr Ser His Thr Pro Leu Val Ile Thr Ala
85 90 95

Gly Gln Gln Val Arg Pro Met Ile Gly Leu Glu Ala Met Leu Ser Asn
100 105 110

Val Asp Ala Ala Ser Leu Pro Arg Pro Leu Val Lys Trp Ser Ala Glu
115 120 125

Pro Ala Gln Ala Pro Asp Val Pro Arg Ala Leu Ser Gln Ala Ile His
130 135 140

Thr Ala Thr Ser Asp Pro Lys Gly Pro Val Tyr Leu Ser Ile Pro Tyr
145 150 155 160

Asp Asp Trp Asn Gln Asp Thr Gly Asn Leu Ser Glu His Leu Ser Ser
165 170 175

Arg Ser Val Ser Arg Ala Gly Asn Pro Ser Ala Glu Gln Leu Asp Asp
180 185 190

Ile Leu Ser Ala Leu Arg Glu Ala Ala Asn Pro Ala Leu Val Phe Gly
195 200 205

Pro Asp Val Asp Ala Ala Arg Ala Asn His His Ala Val Arg Leu Ala
210 215 220

Glu Lys Leu Ala Ala Pro Val Trp Ile Ala Pro Ser Ala Pro Arg Cys
225 230 235 240

Pro Phe Pro Thr Arg His Pro Asn Phe Arg Gly Val Leu Pro Ala Ser
245 250 255

Ile Ala Gly Ile Ser Ala Leu Leu Asn Gly His Asp Leu Ile Val Val
260 265 270

Ile Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Gln Pro Gly Ser Tyr
275 280 285

Leu Pro Glu Asn Ser Arg Leu Ile His Ile Thr Cys Asp Ala Gly Glu
290 295 300

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Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val Ala Asp Ile Gly Gln
 305 310 315 320
 Thr Leu Arg Ala Leu Ala Asp Ile Ile Pro Gln Ser Lys Arg Pro Pro
 325 330 335
 Leu Arg Pro Arg Val Ile Pro Pro Val Pro Asp Ser Gln Asp Asp Leu
 340 345 350
 Leu Ala Pro Asp Ala Val Phe Glu Val Met Asn Glu Val Ala Pro Glu
 355 360 365
 Asp Val Val Tyr Val Asn Glu Ser Thr Ser Thr Val Thr Ala Leu Trp
 370 375 380
 Glu Arg Val Glu Leu Lys His Pro Gly Ser Tyr Tyr Phe Pro Ala Ser
 385 390 395 400
 Gly Gly Leu Gly Phe Gly Met Pro Ala Ala Val Gly Val Gln Leu Ala
 405 410 415
 Asn Asp Arg Arg Arg Val Ile Ala Val Ile Gly Asp Gly Ser Ala Asn
 420 425 430
 Tyr Gly Ile Thr Ala Leu Trp Thr Ala Ala Gln Glu Lys Ile Pro Val
 435 440 445
 Val Phe Ile Ile Leu Asn Asn Gly Thr Tyr Gly Ala Leu Arg Ala Phe
 450 455 460
 Ala Lys Leu Leu Asn Ala Glu Asn Ala Ala Gly Leu Asp Val Pro Gly
 465 470 475 480
 Ile Cys Phe Cys Ala Ile Ala Glu Gly Tyr Gly Val Glu Ala His Arg
 485 490 495
 Ile Thr Ser Leu Glu Asn Phe Lys Asp Lys Leu Ser Ala Ala Leu Gln
 500 505 510
 Ser Asp Thr Pro Thr Leu Leu Glu Val Pro Thr Ser Thr Thr Ser Pro
 515 520 525
 Phe

 <210> SEQ ID NO 28
 <211> LENGTH: 528
 <212> TYPE: PRT
 <213> ORGANISM: Chromohalobacter salexigens

 <400> SEQUENCE: 28

 Met Pro Thr Val His Ser Ala Thr Tyr Asp Leu Leu Arg Arg Gln Gly
 1 5 10 15

 Met Thr Thr Ile Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
 20 25 30

 Lys Asn Phe Pro Ala Asp Phe Arg Tyr Ile Leu Gly Leu His Glu Gly
 35 40 45

 Val Val Val Gly Met Ala Asp Gly Phe Ala Leu Ala Ser Gly Ala Pro
 50 55 60

 Ala Leu Val Asn Leu His Ala Ala Ala Gly Ser Gly Asn Ala Met Gly
 65 70 75 80

 Ala Leu Thr Asn Ala Trp Tyr Ser His Ser Pro Leu Val Leu Thr Ala
 85 90 95

 Gly Gln Gln Ala Arg Ser Met Ile Gly Val Glu Ser Met Leu Ala Asn
 100 105 110

 Val Asp Ala Pro Gln Leu Pro Arg Pro Leu Val Lys Trp Ser Tyr Glu
 115 120 125

 Pro Ala Cys Pro Glu Asp Val Pro Arg Ala Leu Ser Gln Ala Ile His
 130 135 140

Thr Ala Cys Leu Pro Ala Arg Gly Pro Val Tyr Val Ser Ile Pro His
 145 150 155 160
 Asp Asp Trp Gly His Ala Val Asp Asp Asp Ala Ala Leu Leu Ser Ala
 165 170 175
 Arg Gln Val Ala Ser Ala Ala Gln Pro Ala Glu Thr Gln Val Glu Ala
 180 185 190
 Leu Val Glu Arg Leu Asn Ala Ala Arg Asn Pro Val Leu Val Leu Gly
 195 200 205
 Pro Asp Val Asp Ala Tyr Gly Ala Asn Ala Leu Ala Val Thr Leu Ala
 210 215 220
 Glu Arg Leu Asn Ala Pro Ala Trp Val Ala Pro Ser Ala Ser Arg Cys
 225 230 235 240
 Pro Phe Pro Thr Arg His Ala Cys Phe Arg Gly Val Leu Pro Ala Ala
 245 250 255
 Ile Gln Gly Ile Ser Asp Arg Leu Asp Gly His Asp Leu Ile Val Val
 260 265 270
 Ile Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Ala Pro Gly Arg Tyr
 275 280 285
 Leu Pro Asp Gly Ala Glu Leu Val His Leu Thr Cys Asp Met Gln Glu
 290 295 300
 Ala Ala Arg Ala Pro Met Gly Asp Ala Leu Val Gly Asp Ile His Ala
 305 310 315 320
 Met Leu Asp Leu Leu Val Pro Arg Val Arg Gln Ser Gly Arg Ala Arg
 325 330 335
 Pro Glu Pro Gln Ala Ala Pro Glu Pro Gln Val Asp Pro Glu Gly Met
 340 345 350
 Leu Thr Pro Glu Thr Val Phe Asp Val Met Asn Ala Met Ala Pro Glu
 355 360 365
 Asp Ala Ile Tyr Val Lys Glu Ser Thr Ser Thr Val Thr Ala Phe Trp
 370 375 380
 Glu Arg Val Glu Met Arg His Pro Gly Ser Tyr Phe Phe Pro Ala Ala
 385 390 395 400
 Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Val Gln Leu Ala
 405 410 415
 Cys Pro Glu Arg Arg Val Ile Gly Val Ile Gly Asp Gly Ser Ala Asn
 420 425 430
 Tyr Ala Ile Thr Ala Leu Trp Ser Ala Ala Gln Tyr Arg Ile Pro Val
 435 440 445
 Val Phe Val Ile Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
 450 455 460
 Ser Arg Leu Leu Asp Ala Glu Asp Ser Pro Gly Leu Asp Val Pro Gly
 465 470 475 480
 Leu Asp Phe Cys Ala Leu Ala Glu Gly Tyr Gly Val Glu Ala Glu Gln
 485 490 495
 Ala Ala Ser Arg Glu Ala Phe Glu Ala Ala Leu Lys Ala Ala Leu Ala
 500 505 510
 Asp Asp Arg Pro Arg Val Ile Glu Val Pro Thr Thr Ile Glu Pro
 515 520 525

<210> SEQ ID NO 29
 <211> LENGTH: 528
 <212> TYPE: PRT
 <213> ORGANISM: Rhodococcus jostii

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<400> SEQUENCE: 29

Met Ala Thr Val Ser Glu Val Thr Tyr Glu Leu Leu Arg Ala Arg Gly
 1 5 10 15

Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
 20 25 30

Ser Gly Met Pro Asp Asp Phe Arg Tyr Val Leu Gly Leu His Glu Gly
 35 40 45

Ala Val Leu Ser Met Ala Asp Gly Tyr Ser Leu Val Thr Gly Glu Ala
 50 55 60

Thr Leu Val Asn Leu His Ala Ala Ser Gly Ser Gly Asn Ala Met Gly
 65 70 75 80

Ala Leu Thr Asn Ser Val Tyr Ser His Ser Pro Leu Val Val Thr Ala
 85 90 95

Gly Gln Gln Val Arg Ser Thr Ile Gly Gln Glu Val Met Leu Ser Asn
 100 105 110

Val Asp Ala Gly Thr Leu Met Lys Pro Leu Val Lys Trp Ser Ser Glu
 115 120 125

Pro Thr Cys Ala Glu Asp Val Pro Arg Thr Ile Asn Gln Ala Ile His
 130 135 140

Thr Ala Leu Leu Pro Ala Lys Gly Pro Val Tyr Val Ser Val Pro Tyr
 145 150 155 160

Asp Asp Trp Ala Ala Glu Ala Pro Pro Glu Ser Ala Gly Leu Leu Ala
 165 170 175

Arg Glu Val His Ser Ala Ala Ser Leu Ser Gly Asp Gln Ile Asn Asp
 180 185 190

Leu Ile Glu Thr Leu Glu Ser Ala Thr Asn Pro Val Leu Val Leu Gly
 195 200 205

Pro Ala Val Asp Ala Asp Arg Ala Asn Ala Asp Ala Val Leu Leu Ala
 210 215 220

Glu Lys Leu Arg Ala Pro Val Trp Ile Ala Pro Ser Pro Ser Arg Cys
 225 230 235 240

Pro Phe Pro Thr Arg His Pro Ser Phe Arg Gly Val Leu Pro Ala Gly
 245 250 255

Val Ala Asp Leu Ser Lys Thr Leu Glu Gly His Asp Leu Ile Leu Val
 260 265 270

Val Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Val Pro Gly Asn Tyr
 275 280 285

Leu Pro Gly Gly Ala Arg Leu Ile His Val Thr Asp Asp Gly Gly Glu
 290 295 300

Ala Ala Arg Ala Pro Ile Gly Glu Ala Tyr Val Ala Pro Val Gly Ser
 305 310 315 320

Thr Leu Glu Ile Leu Ala Asn Met Val Lys Pro Ser Asp Arg Ser Pro
 325 330 335

Leu Pro Pro Leu Gly Asp Phe Glu Glu Ala Val Ser Val Gly Ala Gly
 340 345 350

Leu Asp Pro Ala Gln Leu Phe Ala Leu Val Arg Ala Gly Ala Pro Asp
 355 360 365

Asp Ala Ile Tyr Val Asn Glu Ser Thr Ser Thr Ser Asp Ala Phe Trp
 370 375 380

Ser Gln Met Asp Leu Ser His Gln Gly Ser Tyr Tyr Phe Pro Ala Ser
 385 390 395 400

Gly Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Ala Gln Leu Ala
 405 410 415

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Ser Pro Asp Arg Gln Val Ile Gly Leu Ile Gly Asp Gly Ser Ala Asn
420 425 430

Tyr Gly Ile Thr Ala Leu Trp Ser Ala Ala Gln Tyr Lys Ile Pro Val
435 440 445

Val Ile Ile Ile Leu Asn Asn Gly Thr Tyr Gly Ala Leu Arg Gly Phe
450 455 460

Ser Lys Ile Leu Asn Thr Gly Glu Thr Pro Gly Leu Asp Val Pro Gly
465 470 475 480

Ile Asp Phe Val His Leu Ala Glu Gly Tyr Gly Val Arg Gly Thr Ala
485 490 495

Val Ala Thr Ala Glu Asp Phe Thr Thr Ala Phe Lys Ser Ala Leu Ala
500 505 510

Ala Asp Ala Pro Thr Leu Ile Glu Val Arg Thr Asn Phe Asp Glu Ser
515 520 525

<210> SEQ_ID NO 30

<211> LENGTH: 527

<212> TYPE: PRT

<213> ORGANISM: Rhodococcus jostii

<400> SEQUENCE: 30

Met Ala Thr Val Ser Glu Val Thr Tyr Glu Leu Leu Arg Ala Arg Gly
1 5 10 15

Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
20 25 30

Ser Gly Met Pro Asp Asp Phe Arg Tyr Val Leu Gly His Glu Gly Ala
35 40 45

Val Leu Ser Met Ala Asp Gly Tyr Ser Leu Val Thr Gly Glu Ala Thr
50 55 60

Leu Val Asn Leu His Ala Ala Ser Gly Ser Gly Asn Ala Met Gly Ala
65 70 75 80

Leu Thr Asn Ser Val Tyr Ser His Ser Pro Leu Val Val Thr Ala Gly
85 90 95

Gln Gln Val Arg Ser Thr Ile Gly Gln Glu Val Met Leu Ser Asn Val
100 105 110

Asp Ala Gly Thr Leu Met Lys Pro Leu Val Lys Trp Ser Ser Glu Pro
115 120 125

Thr Cys Ala Glu Asp Val Pro Arg Thr Ile Asn Gln Ala Ile His Thr
130 135 140

Ala Leu Leu Pro Ala Lys Gly Pro Val Tyr Val Ser Val Pro Tyr Asp
145 150 155 160

Asp Trp Ala Ala Glu Ala Pro Pro Glu Ser Ala Gly Leu Leu Ala Arg
165 170 175

Glu Val His Ser Ala Ala Ser Leu Ser Gly Asp Gln Ile Asn Asp Leu
180 185 190

Ile Glu Thr Leu Glu Ser Ala Thr Asn Pro Val Leu Val Leu Gly Pro
195 200 205

Ala Val Asp Ala Asp Arg Ala Asn Ala Asp Ala Val Leu Leu Ala Glu
210 215 220

Lys Leu Arg Ala Pro Val Trp Ile Ala Pro Ser Pro Ser Arg Cys Pro
225 230 235 240

Phe Pro Thr Arg His Pro Ser Phe Arg Gly Val Leu Pro Ala Gly Val
245 250 255

Ala Asp Leu Ser Lys Thr Leu Glu Gly His Asp Leu Ile Leu Val Val

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260	265	270
Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Val Pro Gly Asn Tyr Leu		
275	280	285
Pro Gly Gly Ala Arg Leu Ile His Val Thr Asp Asp Gly Gly Glu Ala		
290	295	300
Ala Arg Ala Pro Ile Gly Glu Ala Tyr Val Ala Pro Val Gly Ser Thr		
305	310	315
Leu Glu Ile Leu Ala Asn Met Val Lys Pro Ser Asp Arg Ser Pro Leu		
325	330	335
Pro Pro Leu Gly Asp Phe Glu Glu Ala Val Ser Val Gly Ala Gly Leu		
340	345	350
Asp Pro Ala Gln Leu Phe Ala Leu Val Arg Ala Gly Ala Pro Asp Asp		
355	360	365
Ala Ile Tyr Val Asn Glu Ser Thr Ser Thr Ser Asp Ala Phe Trp Ser		
370	375	380
Gln Met Asp Leu Ser His Gln Gly Ser Tyr Tyr Phe Pro Ala Ser Gly		
385	390	395
Gly Leu Gly Phe Gly Leu Pro Ala Ala Val Gly Ala Gln Leu Ala Ser		
405	410	415
Pro Asp Arg Gln Val Ile Gly Leu Ile Gly Asp Gly Ser Ala Asn Tyr		
420	425	430
Gly Ile Thr Ala Leu Trp Ser Ala Ala Gln Tyr Lys Ile Pro Val Val		
435	440	445
Ile Ile Ile Leu Asn Asn Gly Thr Tyr Gly Ala Leu Arg Gly Phe Ser		
450	455	460
Lys Ile Leu Asn Thr Gly Glu Thr Pro Gly Leu Asp Val Pro Gly Ile		
465	470	475
Asp Phe Val His Leu Ala Glu Gly Tyr Gly Val Arg Gly Thr Ala Val		
485	490	495
Ala Thr Ala Glu Asp Phe Thr Thr Ala Phe Lys Ser Ala Leu Ala Ala		
500	505	510
Asp Ala Pro Thr Leu Ile Glu Val Arg Thr Asn Phe Asp Glu Ser		
515	520	525
<210> SEQ_ID NO 31		
<211> LENGTH: 476		
<212> TYPE: PRT		
<213> ORGANISM: Saccharopolyspora erythraea		
<400> SEQUENCE: 31		
Met Ala Asp Gly Tyr Ala Leu Ala Arg Gly Gly Pro Ala Leu Val Asn		
1 5 10 15		
Leu His Ala Ala Ala Gly Thr Gly Asn Ala Leu Gly Ala Leu Thr Asn		
20 25 30		
Ser Val Tyr Ser His Ser Pro Leu Val Ile Thr Ala Gly Gln Gln Val		
35 40 45		
Arg Ser Thr Ile Gly Gln Glu Val Met Leu Ala Asn Val Asp Ala Ala		
50 55 60		
Ser Leu Pro Lys Pro Leu Val Lys Trp Ser Ala Glu Pro Ser Cys Ala		
65 70 75 80		
Gln Asp Val Pro Arg Thr Ile Ser Gln Ala Ile His Thr Ala Asn Leu		
85 90 95		
Pro Ala Lys Gly Pro Val Tyr Val Ser Val Pro Tyr Asp Asp Trp Asp		
100 105 110		

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Gly Glu Ala Pro Arg Glu Ala Gly His Leu Leu Arg Arg Ser Thr Thr
115 120 125

Ser Ala Gly Ser Leu Gly Ser Glu Gln Leu Ala Asp Leu Val Gln Ala
130 135 140

Val Asp Ser Ala Arg Asn Pro Val Leu Val Leu Gly Pro Asp Val Asp
145 150 155 160

Ala Gln His Ala Asn Asp His Ala Val Arg Leu Ala Asp Lys Leu Asn
165 170 175

Ala Pro Val Trp Val Ala Pro Ser Pro Ser Arg Cys Pro Phe Pro Thr
180 185 190

Arg His Arg Ser Phe Arg Gly Val Leu Pro Ala Ala Val Gln Gly Val
195 200 205

Thr Asp Ala Leu Asp Gly His Asp Leu Val Leu Val Ala Gly Ala Pro
210 215 220

Val Phe Arg Tyr His Gln Tyr Val Pro Gly Glu Tyr Leu Pro Glu Gly
225 230 235 240

Ala Arg Leu Val His Leu Thr Ser Asp Pro Gly Glu Ala Ala Arg Ala
245 250 255

Pro Met Gly Glu Ala Leu Val Cys Asp Ile Ala Asp Ala Leu Ser Arg
260 265 270

Leu Ala Asp Glu Ala Ala Asp Thr Asp Arg Pro Arg Leu Pro Pro Leu
275 280 285

Pro Asp Phe Pro Ser Val Ser Gly Ser Gly Gly Ala Val His Pro Ala
290 295 300

Glu Leu Phe Ala Thr Leu Arg Asp Ile Ala Pro Glu Asp Ala Val Tyr
305 310 315 320

Val Lys Glu Ser Thr Ala Thr Thr Gly Thr Phe Trp Ser Gln Met Asp
325 330 335

Leu Ser Arg Gln Gly Ser Tyr Phe Phe Pro Ala Ser Gly Gly Leu Gly
340 345 350

Phe Gly Leu Pro Ala Ala Val Gly Ala Gln Leu Ala His Pro Glu Arg
355 360 365

Gln Val Val Gly Leu Ile Gly Asp Gly Ser Ala Asn Tyr Gly Ile Thr
370 375 380

Ala Leu Trp Thr Ala Ala Gln Tyr Arg Ile Pro Val Ser Ile Val Ile
385 390 395 400

Leu Lys Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe Ala Lys Val Leu
405 410 415

Asp Ala Gly Glu Thr Pro Gly Met Asp Val Pro Gly Ile Asp Phe Val
420 425 430

Arg Ile Ala Gly Gly Tyr Gly Val Glu Ala Thr Ser Val Arg Thr Ala
435 440 445

Ala Asp Phe Ala Thr Ala Phe Glu Asp Ala Leu Gly Ala Gly Arg Pro
450 455 460

Ala Leu Ile Glu Val Glu Thr Glu Leu Thr Glu Pro
465 470 475

<210> SEQ ID NO 32
<211> LENGTH: 526
<212> TYPE: PRT
<213> ORGANISM: Streptomyces lividans

<400> SEQUENCE: 32

Met Pro Ser Val Arg Arg Val Ser His Glu Phe Leu Glu Arg Gln Gly
1 5 10 15

-continued

Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
 20 25 30

Ala Gly Leu Pro Asp Gly Phe Arg Tyr Val Leu Gly Leu His Glu Gly
 35 40 45

Ala Val Val Gly Met Ala Asp Gly Tyr Ala Gln Ala Thr Gly Arg Pro
 50 55 60

Val Leu Val Asn Leu His Ala Ala Ser Gly Ser Gly Asn Ala Met Gly
 65 70 75 80

Ala Leu Thr Asn Ala Val Ala Ser Arg Thr Pro Leu Val Val Ala
 85 90 95

Gly Gln Gln Val Arg Pro Ala Ile Gly Pro Glu Ala Asn Leu Ala Ser
 100 105 110

Val Asp Ala Pro Ala Leu Met Lys Pro Leu Val Gly Trp Ala Ala Glu
 115 120 125

Pro Ala Cys Ala Gly Asp Val Pro Arg Ala Leu Ala Gln Ala Val Phe
 130 135 140

Glu Ala Arg Leu Gln Arg Arg Pro Thr Tyr Leu Ser Val Pro Tyr Asp
 145 150 155 160

Asp Trp Ser Ala Asp Val Asp Asn Ala Leu Ala Val Leu Asp Arg
 165 170 175

Arg Val Leu Arg Ala Ala Val Pro Gly Gly Glu Gln Arg Arg Trp Leu
 180 185 190

Val Glu Gln Val Ala Ser Ala Arg Arg Pro Ala Leu Val Leu Gly Gly
 195 200 205

Asp Ile Asp Ser Ala Gly Arg Phe Asp Asp Ala Val Arg Leu Ala Glu
 210 215 220

Arg Leu Gly Gly Pro Val Trp Ala Ala Pro Ser Gln Phe Arg Leu Pro
 225 230 235 240

Phe Pro Asn Arg His Pro Leu Phe Arg Gly Val Leu Pro Ala Gly Ile
 245 250 255

Ala Pro Val Ser Ala Ala Phe Glu Gly His Asp Leu Val Leu Val Leu
 260 265 270

Gly Ala Pro Val Phe Arg Tyr His Glu His Leu Pro Gly Arg Tyr Leu
 275 280 285

Pro Glu Gly Thr Arg Leu Ile Gln Val Thr Glu Asp Ala Ser Ala Ala
 290 295 300

Ala Arg Ala Pro Met Gly Glu Ala Leu Val Ala Asp Pro Gly Ala Val
 305 310 315 320

Ile Asp Ile Leu Leu Glu Ala Leu Gly Ala Ala Asp Arg Pro Ala Gly
 325 330 335

Pro Tyr Arg Pro Val Pro Glu Pro Leu Thr Ala Glu Gly Pro Ala Leu
 340 345 350

His Pro Glu Gln Val Phe Ala Ala Leu Arg Glu Glu Met Pro Glu Asp
 355 360 365

Thr Ala Tyr Val Val Glu Ser Thr Ser Thr Asn Ala Ala Trp Trp Arg
 370 375 380

Gln Thr Asp Leu Arg Arg Gln Gly Ser Tyr Tyr Phe Pro Ala Ala Gly
 385 390 395 400

Gly Leu Gly Phe Gly Leu Pro Gly Ala Val Gly Val Ala Met Ala Gln
 405 410 415

Pro Gly Arg Pro Val Val Gly Val Ile Gly Asp Gly Ser Ala Asn Tyr
 420 425 430

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Gly Ile Thr Ala Leu Trp Thr Ala Ala Gln His Arg Val Pro Leu Thr
435 440 445

Val Val Leu Leu Arg Asn Gly Ala Tyr Gly Ala Leu Arg Trp Phe Gly
450 455 460

Gly Leu Leu Gly Val Pro Asp Ala Pro Gly Leu Asp Ile Pro Gly Leu
465 470 475 480

Asp Phe Thr Arg Ile Ala Glu Gly Tyr Gly Val Arg Ala Gln His Val
485 490 495

Gly Ser Val Ala Glu Leu Arg Ala Ala Leu Ala Glu Thr Pro Glu His
500 505 510

Pro Arg Leu Ile Gln Val Asp Thr Ala Leu Thr Thr Pro Ser
515 520 525

<210> SEQ_ID NO 33

<211> LENGTH: 526

<212> TYPE: PRT

<213> ORGANISM: Streptomyces coelicolor

<400> SEQUENCE: 33

Met Pro Ser Val Arg Arg Val Ser His Glu Phe Leu Glu Arg Gln Gly
1 5 10 15

Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
20 25 30

Ala Gly Leu Pro Asp Gly Phe Arg Tyr Val Leu Gly Leu His Glu Gly
35 40 45

Ala Val Val Gly Met Ala Asp Gly Tyr Ala Gln Ala Thr Gly Arg Pro
50 55 60

Val Leu Val Asn Leu His Ala Ala Ser Gly Ser Gly Asn Ala Met Gly
65 70 75 80

Ala Leu Thr Asn Ala Val Ala Ser Arg Thr Pro Leu Val Val Ala
85 90 95

Gly Gln Gln Val Arg Pro Ala Ile Gly Pro Glu Ala Asn Leu Ala Ser
100 105 110

Val Asp Ala Pro Ala Leu Met Lys Pro Leu Val Gly Trp Ala Ala Glu
115 120 125

Pro Ala Cys Ala Gly Asp Val Pro Arg Ala Leu Ala Gln Ala Val Phe
130 135 140

Glu Ala Arg Leu Gln Arg Arg Pro Thr Tyr Leu Ser Val Pro Tyr Asp
145 150 155 160

Asp Trp Ser Ala Asp Val Asp Asn Ala Leu Ala Val Leu Asp Arg
165 170 175

Arg Val Leu Arg Ala Ala Val Pro Gly Gly Glu Gln Arg Arg Trp Leu
180 185 190

Val Glu Gln Val Ala Ser Ala Arg Arg Pro Ala Leu Val Leu Gly Gly
195 200 205

Asp Ile Asp Ser Ala Gly Arg Phe Asp Asp Ala Val Arg Leu Ala Glu
210 215 220

Arg Leu Gly Gly Pro Val Trp Ala Ala Pro Ser Gln Phe Arg Leu Pro
225 230 235 240

Phe Pro Asn Arg His Pro Leu Phe Arg Gly Val Leu Pro Ala Gly Ile
245 250 255

Ala Pro Val Ser Ala Ala Phe Glu Gly His Asp Leu Val Leu Val Leu
260 265 270

Gly Ala Pro Val Phe Arg Tyr His Glu His Leu Pro Gly Arg Tyr Leu
275 280 285

-continued

Pro Glu Gly Thr Arg Leu Ile Gln Val Thr Glu Asp Ala Ser Ala Ala
290 295 300

Ala Arg Ala Pro Met Gly Glu Ala Leu Val Ala Asp Pro Gly Ala Val
305 310 315 320

Ile Asp Val Leu Leu Glu Ala Leu Gly Ala Ala Asp Arg Pro Ala Gly
325 330 335

Pro Tyr Arg Pro Val Pro Glu Pro Leu Thr Ala Glu Gly Pro Ala Leu
340 345 350

His Pro Glu Gln Val Phe Ala Ala Leu Arg Glu Glu Met Pro Glu Asp
355 360 365

Thr Ala Tyr Val Val Glu Ser Thr Ser Thr Asn Ala Ala Trp Trp Arg
370 375 380

Gln Thr Asp Leu Arg Arg Gln Gly Ser Tyr Tyr Phe Pro Ala Ala Gly
385 390 395 400

Gly Leu Gly Phe Gly Leu Pro Gly Ala Val Gly Val Ala Met Ala Gln
405 410 415

Pro Gly Arg Pro Val Val Gly Val Ile Gly Asp Gly Ser Ala Asn Tyr
420 425 430

Gly Ile Thr Ala Leu Trp Thr Ala Ala Gln His Arg Val Pro Leu Thr
435 440 445

Val Val Leu Leu Arg Asn Gly Ala Tyr Gly Ala Leu Arg Trp Phe Gly
450 455 460

Gly Leu Leu Gly Val Pro Asp Ala Pro Gly Leu Asp Ile Pro Asp Leu
465 470 475 480

Asp Phe Thr Arg Ile Ala Glu Gly Tyr Gly Val Arg Ala Gln His Val
485 490 495

Gly Ser Val Ala Glu Leu Arg Ala Ala Leu Ala Glu Thr Pro Glu His
500 505 510

Pro Arg Leu Ile Gln Val Asp Thr Ala Leu Thr Thr Pro Ser
515 520 525

<210> SEQ_ID NO 34

<211> LENGTH: 523

<212> TYPE: PRT

<213> ORGANISM: Streptomyces lividans

<400> SEQUENCE: 34

Met Arg Arg Val Ser His Glu Phe Leu Glu Arg Gln Gly Leu Thr Thr
1 5 10 15Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu Ala Gly Leu
20 25 30Pro Asp Gly Phe Arg Tyr Val Leu Gly Leu His Glu Gly Ala Val Val
35 40 45Gly Met Ala Asp Gly Tyr Ala Gln Ala Thr Gly Arg Pro Val Leu Val
50 55 60Asn Leu His Ala Ala Ser Gly Ser Gly Asn Ala Met Gly Ala Leu Thr
65 70 75 80Asn Ala Val Ala Ser Arg Thr Pro Leu Val Val Ala Gly Gln Gln
85 90 95Val Arg Pro Ala Ile Gly Pro Glu Ala Asn Leu Ala Ser Val Asp Ala
100 105 110Pro Ala Leu Met Lys Pro Leu Val Gly Trp Ala Ala Glu Pro Ala Cys
115 120 125

Ala Gly Asp Val Pro Arg Ala Leu Ala Gln Ala Val Phe Glu Ala Arg

-continued

130	135	140
Leu Gln Arg Arg Pro Thr Tyr Leu Ser Val Pro Tyr Asp Asp Trp Ser		
145	150	155
160		
Ala Asp Val Asp Asp Asn Ala Leu Ala Val Leu Asp Arg Arg Val Leu		
165	170	175
Arg Ala Ala Val Pro Gly Gly Glu Gln Arg Arg Trp Leu Val Glu Gln		
180	185	190
Val Ala Ser Ala Arg Arg Pro Ala Leu Val Leu Gly Gly Asp Ile Asp		
195	200	205
Ser Ala Gly Arg Phe Asp Asp Ala Val Arg Leu Ala Glu Arg Leu Gly		
210	215	220
Gly Pro Val Trp Ala Ala Pro Ser Gln Phe Arg Leu Pro Phe Pro Asn		
225	230	235
240		
Arg His Pro Leu Phe Arg Gly Val Leu Pro Ala Gly Ile Ala Pro Val		
245	250	255
Ser Ala Ala Phe Glu Gly His Asp Leu Val Leu Val Leu Gly Ala Pro		
260	265	270
Val Phe Arg Tyr His Glu His Leu Pro Gly Arg Tyr Leu Pro Glu Gly		
275	280	285
Thr Arg Leu Ile Gln Val Thr Glu Asp Ala Ser Ala Ala Ala Arg Ala		
290	295	300
Pro Met Gly Glu Ala Leu Val Ala Asp Pro Gly Ala Val Ile Asp Ile		
305	310	315
320		
Leu Leu Glu Ala Leu Gly Ala Ala Asp Arg Pro Ala Gly Pro Tyr Arg		
325	330	335
Pro Val Pro Glu Pro Leu Thr Ala Glu Gly Pro Ala Leu His Pro Glu		
340	345	350
Gln Val Phe Ala Ala Leu Arg Glu Glu Met Pro Glu Asp Thr Ala Tyr		
355	360	365
Val Val Glu Ser Thr Ser Thr Asn Ala Ala Trp Trp Arg Gln Thr Asp		
370	375	380
Leu Arg Arg Gln Gly Ser Tyr Tyr Phe Pro Ala Ala Gly Gly Leu Gly		
385	390	395
400		
Phe Gly Leu Pro Gly Ala Val Gly Val Ala Met Ala Gln Pro Gly Arg		
405	410	415
Pro Val Val Gly Val Ile Gly Asp Gly Ser Ala Asn Tyr Gly Ile Thr		
420	425	430
Ala Leu Trp Thr Ala Ala Gln His Arg Val Pro Leu Thr Val Val Leu		
435	440	445
Leu Arg Asn Gly Ala Tyr Gly Ala Leu Arg Trp Phe Gly Gly Leu Leu		
450	455	460
Gly Val Pro Asp Ala Pro Gly Leu Asp Ile Pro Gly Leu Asp Phe Thr		
465	470	475
480		
Arg Ile Ala Glu Gly Tyr Gly Val Arg Ala Gln His Val Gly Ser Val		
485	490	495
Ala Glu Leu Arg Ala Ala Leu Ala Glu Thr Pro Glu His Pro Arg Leu		
500	505	510
Ile Gln Val Asp Thr Ala Leu Thr Thr Pro Ser		
515	520	

<210> SEQ ID NO 35

<211> LENGTH: 526

<212> TYPE: PRT

<213> ORGANISM: Streptomyces ambofaciens

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<400> SEQUENCE: 35

Met Pro Ser Val Arg Arg Val Ser His Ala Phe Leu Glu Arg Gln Gly
1 5 10 15

Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
20 25 30

Ala Asp Leu Pro Asp Gly Phe Arg Tyr Val Leu Gly Leu His Glu Gly
35 40 45

Ala Val Val Gly Met Ala Asp Gly Tyr Ala Gln Ala Thr Gly Arg Pro
50 55 60

Val Leu Val Asn Leu His Ala Ala Ser Gly Ser Gly Asn Ala Met Gly
65 70 75 80

Ala Leu Thr Asn Ala Val Ala Ser Arg Thr Pro Leu Val Val Ala
85 90 95

Gly Gln Gln Val Arg Pro Ala Ile Gly Pro Glu Ala Asn Leu Ala Ser
100 105 110

Val Asp Ala Gln Thr Leu Met Lys Pro Leu Val Gly Trp Ala Ala Glu
115 120 125

Pro Ala Cys Ala Glu Asp Val Pro Arg Ala Leu Ala Gln Ala Val Phe
130 135 140

Glu Ala Arg Leu Gln Arg Arg Pro Thr Tyr Leu Ser Val Pro Tyr Asp
145 150 155 160

Asp Trp Ser Ala Glu Val Asp Asp Asn Ala Leu Ala Val Leu Asp Arg
165 170 175

Arg Val Glu Arg Ala Ser Val Pro Asp Ala Val Gln Ser Arg Arg Leu
180 185 190

Ala Glu Arg Val Ala Ala Arg Arg Pro Ala Leu Val Leu Gly Gly
195 200 205

Asp Ile Asp Ser Pro Gly Leu Phe Asp Asp Ala Val Arg Leu Ala Glu
210 215 220

Arg Leu Gly Cys Pro Val Trp Ala Ala Pro Ser Leu Phe Arg Leu Pro
225 230 235 240

Phe Pro Asn Arg His Pro Gln Phe Arg Gly Val Leu Pro Ala Gly Ile
245 250 255

Ala Pro Val Cys Glu Ala Phe Glu Gly His Asp Leu Val Leu Val Leu
260 265 270

Gly Ala Pro Val Phe Arg Tyr His Glu Tyr Leu Pro Gly Arg Tyr Leu
275 280 285

Pro Glu Gly Thr Arg Leu Val Gln Val Thr Asp Asp Ala Ser Ala Ala
290 295 300

Ala Arg Ala Pro Met Gly Glu Ala Leu Val Ala Asp Pro Gly Ala Val
305 310 315 320

Val Gly Leu Leu Leu Arg Ser Leu Asp Ala Pro Gly Glu Pro Ala Gly
325 330 335

Pro Tyr Arg Pro Ala Pro Glu Pro Leu Thr Ala Gly Gly Pro Ser Leu
340 345 350

His Pro Glu Gln Val Phe Ala Ala Leu Arg Glu Gly Leu Pro Ala Asp
355 360 365

Thr Ala Tyr Val Val Glu Ser Thr Ser Thr Asn Ser Ala Trp Trp Arg
370 375 380

Gln Met Asp Leu Arg Arg Pro Gly Ser Tyr Tyr Phe Pro Ala Ala Gly
385 390 395 400

Gly Leu Gly Phe Gly Leu Pro Gly Ala Val Gly Val Ala Met Ala Gln

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405	410	415
Pro Asp Arg Pro Val Val Gly Val Ile Gly Asp Gly Ser Ala Asn Tyr		
420	425	430
Gly Ile Thr Ala Leu Trp Thr Ala Ala Gln His Gly Val Pro Leu Thr		
435	440	445
Ile Val Leu Leu Arg Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe Gly		
450	455	460
Gly Leu Leu Gly Val Pro Asp Ala Pro Gly Leu Asp Ile Pro Gly Leu		
465	470	475
Asp Phe Thr Arg Val Ala Glu Gly Tyr Gly Val Arg Ala Arg His Val		
485	490	495
Gly Gly Val Glu Glu Leu Arg Ala Val Leu Ala Glu Gln Pro Gly His		
500	505	510
Pro Arg Leu Ile Gln Val Asp Thr Ala Leu Thr Thr Pro Ser		
515	520	525

<210> SEQ_ID NO 36

<211> LENGTH: 538

<212> TYPE: PRT

<213> ORGANISM: Streptomyces sp.

<400> SEQUENCE: 36

Met Leu Arg Thr Ala Gly Glu Glu Ser Gly Val Lys Val Arg Asp Ala		
1	5	10
Phe Phe Glu Val Leu Arg Ser His Gly Ile Thr Thr Val Phe Gly Asn		
20	25	30
Pro Gly Ser Asn Glu Leu Pro Leu Leu Arg Asp Phe Pro Asp Asp Phe		
35	40	45
Arg Tyr Val Leu Ala Leu His Glu Gly Ala Ala Ile Ala Met Ala Asp		
50	55	60
Gly Tyr Ala Leu Ala Thr Gly Arg Pro Ser Leu Val Asn Leu His Ala		
65	70	75
Ala Ala Gly Thr Gly Asn Ala Met Gly Asn Leu Thr Asn Thr Gln Ser		
85	90	95
Gly His Val Pro Val Val Val Thr Ser Gly Gln Gln Ala Arg Arg Tyr		
100	105	110
Thr Ala Leu Asn Ala Leu Leu Thr Asn Val Asp Ala Thr Ala Leu Ala		
115	120	125
Glu Pro Leu Val Lys Trp Ser Cys Glu Pro Leu Arg Pro Glu Asp Val		
130	135	140
Pro Gln Ala Leu Ser Gln Gly Ile Leu Ala Gly Ser Ala Pro Ala		
145	150	155
Gly Pro Val Tyr Leu Ser Leu Pro Leu Asp Asp Trp Asp His Gln Ala		
165	170	175
Asp Pro Gly Ala Leu Lys His Leu Lys Ala Arg Thr Val Gln Gly Asp		
180	185	190
Pro Val Val Ser Glu Pro Ala Leu Asp Leu Leu Arg Arg Arg Leu Thr		
195	200	205
Gly Ala Ala Asn Pro Val Met Val Val Gly Pro Gly Ile Asp Asp Ala		
210	215	220
Thr Gly Trp Asp Gly Ala Cys Arg Leu Ala Asp Arg Leu Ala Leu Pro		
225	230	235
Val Phe Val Ala Pro Ser Pro Ser Arg Cys Pro Phe Pro Thr Arg His		
245	250	255

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Pro Gly Tyr Arg Gly Val Leu Pro Ser Asp Ile Pro Ala Val Ala Arg
260 265 270

His Phe Asp Gly His Asp Leu Val Val Ala Phe Gly Ala Ala Ile Phe
275 280 285

Arg Tyr His Ala Phe Glu Glu Gly Asp Tyr Leu Pro Pro Gly Thr Glu
290 295 300

Leu Trp Ala Val Thr Ser Asp Pro Asp Glu Ala Thr Arg Ala Pro Phe
305 310 315 320

Gly Arg Ile Leu Val Gly Asn Pro Ser Asp Ala Leu Ala Arg Leu Thr
325 330 335

Glu Thr Val Pro Ala Arg His Arg Pro Pro Pro Pro Leu Glu Arg
340 345 350

Thr Ser Arg Leu Asn Glu Ala Gly Pro Ala Phe Ser Ala Glu Ala Ile
355 360 365

Val Asp Ala Leu Asp Ala Ala Lys Asp Glu Ser Thr Val Leu Ala His
370 375 380

Glu Trp Thr Ser Val Asp Thr Thr Trp Asp Arg Phe Asp Ile Ser Arg
385 390 395 400

Pro Gly Ser Leu Tyr Phe Pro Ala Ser Gly Gly Leu Gly Trp Gly Leu
405 410 415

Pro Ala Ala Ile Gly Leu Gln Leu Gly Asp Pro Ser Arg Arg Val Leu
420 425 430

Ala Met Leu Gly Asp Gly Ala Leu His Tyr Thr Val Ser Ala Leu Trp
435 440 445

Thr Ala Ala Arg Tyr Arg Val Pro Val Val Phe Val Val Ala Arg Asn
450 455 460

Gly Glu Tyr Gly Ala Leu Lys Lys Phe Thr Gln Ala Met Gln Ala Pro
465 470 475 480

Gly Val Pro Gly Leu Glu Leu Pro Gly Ile Asp Ile Thr Gly Ile Ala
485 490 495

Ser Ala Tyr Gly Ile Ser Ala Thr Arg Ile Asp Thr Leu Asp Ala Leu
500 505 510

Thr Ala Ala Val Thr Ala Ala Leu Ala Thr Asp Glu Pro His Leu Ile
515 520 525

Glu Val Pro Gln Gln Pro Leu Thr Ala Ser
530 535

<210> SEQ ID NO 37
<211> LENGTH: 535
<212> TYPE: PRT
<213> ORGANISM: Brevibacterium linens

<400> SEQUENCE: 37

Met Thr Ala Thr Gly Lys Thr Val Leu Gln Ala Ser Leu Asp Val Phe
1 5 10 15

Arg Thr His Gly Met Thr Thr Ile Phe Gly Asn Pro Gly Ser Asn Glu
20 25 30

Leu Pro Phe Leu Ala Gly Leu Gly Asp Asp Phe Arg Phe Val Leu Gly
35 40 45

Leu His Glu Gln Val Val Val Gly Met Ala Glu Gly Phe Ala Arg Ala
50 55 60

Thr Gly Arg Pro Val Leu Val Asn Leu His Ala Ala Ser Gly Ser Gly
65 70 75 80

Asn Gly Met Gly Ala Leu Thr Asn Ala His Tyr Gly His Val Pro Leu
85 90 95

Val Val Leu Ala Gly Gln Gln Val Arg Arg Thr Val Gly Gln Glu Thr
 100 105 110
 Met Leu Ala Ser Ala Asp Ala Ala Thr Leu Pro Thr Pro Leu Val Lys
 115 120 125
 Tyr Ser His Glu Pro Leu Ser Ala Thr Asp Val Pro Arg Thr Leu Ser
 130 135 140
 Gln Ala Ala Phe Glu Ala Thr Thr Gln Pro Ser Gly Pro Val Tyr Val
 145 150 155 160
 Ser Val Pro Leu Asp Asp Trp Asp Glu Glu Ala Leu Asp Asp Asp Asp
 165 170 175
 Leu Leu Thr Thr Arg Thr Val Ser Thr Gly Arg Gly Leu Asp Pro Gln
 180 185 190
 Leu Gln Glu Glu Leu Leu Ala Ser Leu Asp Gly Ala Lys Arg Pro Ala
 195 200 205
 Leu Val Val Gly Pro Gln Val Asp Ala Ala Ala Val Ser Asp Pro Glu
 210 215 220
 Val Leu Glu Ala Val Gln Ala Leu Ala Glu Lys Leu Asp Ala Ser Val
 225 230 235 240
 Tyr Val Ala Pro Ser Pro Thr Arg Cys Pro Phe Pro Thr Thr His Pro
 245 250 255
 Asn Phe Glu Gly Val Met Val Pro Gly Ile Gly Ser Val Arg Asp Arg
 260 265 270
 Leu Ala Asp His Asp Val Val Leu Val Leu Gly Ala Ala Val Phe Arg
 275 280 285
 Tyr His Arg Trp Glu Pro Ser Asn Tyr Leu Ser Pro Gly Thr Glu Val
 290 295 300
 Ile Gln Ile Thr Gln Asp Pro Arg Glu Ala Thr Arg Ala Pro Phe Gly
 305 310 315 320
 Arg Ala Val Ile Thr Asp Val Ala Ser Thr Ala Ala Thr Leu Ala Asp
 325 330 335
 Gly Val Thr Asp Arg Gly Thr Arg Arg Gly Glu Arg Gly Ser Arg Ile
 340 345 350
 Met Ser Pro Ala Ala Thr Ser Ala Glu Gly Met Thr Gly Glu Ile
 355 360 365
 Leu Glu Val Leu Asn Glu His Val Asn Asp Ser Val Ser Tyr Val Asn
 370 375 380
 Glu Thr Thr Leu Asp Leu Asp Tyr Leu Glu Arg Val Ala Ile Asp
 385 390 395 400
 Arg Pro Gly Met Tyr Ser Phe Pro Ala Ser Gly Gly Leu Gly Phe Gly
 405 410 415
 Leu Pro Val Ala Val Gly Met Ser Ile Gly Ala Pro Glu Asn Thr Val
 420 425 430
 Val Ala Thr Val Gly Asp Gly Ser Ala Asn Tyr Gly Ile Thr Ala Leu
 435 440 445
 Tyr Thr Ala Ala Gln Leu Gln Thr Arg Thr Val Phe Val Ile Ile Asn
 450 455 460
 Asn Ser Gly Tyr Gly Ala Leu Ala Gly Phe Ala Gln Arg Met Gly Val
 465 470 475 480
 Pro Lys Val Pro Gly Leu Ala Leu Gly Gly Ile Asp Phe Val Ser Leu
 485 490 495
 Ala Lys Gly Tyr Gly Val Pro Ala Lys Gln Thr Ser Thr Arg Ala Glu
 500 505 510

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Phe Ala Ala Ala Tyr Arg Glu Ala Leu Asp Ala Thr Gly Pro Val Leu
515 520 525

Ile Asp Ala Ser Ile Val Ser
530 535

<210> SEQ ID NO 38

<211> LENGTH: 537

<212> TYPE: PRT

<213> ORGANISM: Mycobacterium smegmatis str.

<400> SEQUENCE: 38

Met Ser Asp Gln Lys Thr Val His Asp Val Thr Tyr Asp Leu Leu Arg
1 5 10 15

Lys Leu Gly Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Thr Glu Glu
20 25 30

Ser Phe Leu Arg Asp Phe Pro Glu Asp Phe Thr Tyr Val Leu Ser Leu
35 40 45

Gln Glu Ala Ser Ala Leu Ala Met Ala Asp Gly Phe Ala Gln Ala Thr
50 55 60

Gly Lys Pro Ala Leu Val Asn Leu His Thr Ala Ala Gly Thr Gly Asn
65 70 75 80

Ala Met Gly Ser Leu Val Ala Ala Tyr Arg Ala Asn Thr Pro Leu Ile
85 90 95

Ile Thr Ala Gly Gln Gln Thr Arg Glu Met Ser Val Val Asp Pro Tyr
100 105 110

Leu Asn Asn Pro Asp Ala Thr Thr Met Pro Lys Pro Trp Val Lys Trp
115 120 125

Ser Tyr Glu Pro Ala Arg Ala Glu Asp Val Pro Ala Ala Phe Met Gln
130 135 140

Ala Tyr Ala Val Ala Met Gln Pro Pro Met Gly Pro Val Phe Leu Ser
145 150 155 160

Ile Pro Leu Asp Asp Trp Asp Lys Pro Ala Leu Gly Pro Ala Ala Val
165 170 175

Arg Ser Val Ser Thr Arg Val Ala Pro Asp Ala Glu Arg Leu Ala Gln
180 185 190

Phe Ala Glu Arg Ile Asn Ala Ala Lys His Pro Met Leu Val Leu Gly
195 200 205

Pro Glu Val Asp Arg Ala Gly Ala Trp Asp Ala Gly Ile Glu Phe Ala
210 215 220

Glu Lys Leu Gly Ala Pro Val His Ala Ser Ala Leu Pro Asp Arg Met
225 230 235 240

Ser Phe Pro Glu Asp His Pro Leu Tyr Ala Gly Pro Leu Pro Met Thr
245 250 255

Ile Ala Gly Val Glu Gln Ala Val Ser Ala Tyr Asp Leu Val Val Val
260 265 270

Val Gly Ala Glu Val Phe Arg Tyr Tyr Pro Tyr Val Pro Gly Glu Tyr
275 280 285

Leu Pro Glu Gly Thr Asp Leu Leu Gln Ile Thr Ala Asp Pro His Arg
290 295 300

Ser Ala Val Ala Pro Val Gly Asp Ser Leu Val Gly Asp Val Gly Ile
305 310 315 320

Ala Leu Ser Arg Leu Thr Glu Leu Ile Asp Thr Pro Asp Asp Arg Val
325 330 335

Pro Pro Lys Pro Leu Val Arg Gln Arg His Ser Asp Ile Pro Ser Thr
340 345 350

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Ala Pro Met Thr Ser Asn Ala Val Tyr Glu Val Leu Ser Asn Val Lys
 355 360 365
 Pro Asp Asp Ala Ala Val Val Met Glu Ser Thr Ser Thr Met Leu Asp
 370 375 380
 Leu Phe Thr Trp Leu Pro Thr Thr His Pro Ala Ser Phe Phe Ala Thr
 385 390 395 400
 Gly Ser Gly Gly Ile Gly Trp Gly Val Pro Ala Ala Val Gly Ile Ala
 405 410 415
 Leu Gly Asp Arg Ala Arg Gly Val Asp Arg Thr Val Val Ala Thr Ile
 420 425 430
 Gly Asp Gly Ser Phe Gln Tyr Ser Ile Gln Ala Ile Trp Thr Ala Ala
 435 440 445
 Gln His Lys Leu Pro Ile Val Phe Val Val Leu Arg Asn Gly Glu Tyr
 450 455 460
 Ala Ile Leu Lys Ser Phe Ala Asp Leu Glu Lys Thr Pro Asn Val Pro
 465 470 475 480
 Gly Leu Gln Leu Pro Gly Leu Asp Ile Ser Ser Ile Ala Ala Gly Phe
 485 490 495
 Gly Cys Arg Thr Ala Thr Val Glu Ser Thr Asp Met Leu Glu Ala Glu
 500 505 510
 Leu Lys Thr Ala Leu Gln Ala Asp Gly Pro Thr Val Leu Val Val Pro
 515 520 525
 Thr Leu Pro Gln Leu Pro Gln Leu Gly
 530 535

<210> SEQ ID NO 39
 <211> LENGTH: 543
 <212> TYPE: PRT
 <213> ORGANISM: Providencia rustigianii

<400> SEQUENCE: 39

Met Lys Lys Thr Ile Arg Gln Val Thr Phe Asp Leu Leu Arg Glu Leu
 1 5 10 15
 Asp Ile Thr Thr Ile Phe Gly Asn Pro Gly Ser Thr Glu Glu Thr Phe
 20 25 30
 Leu Lys Asp Phe Pro Ser Asp Phe Arg Tyr Ile Gln Thr Leu His Glu
 35 40 45
 Ala Ser Ala Val Ala Ala Ala Asp Gly Tyr Ala Gln Gly Met Arg Lys
 50 55 60
 Val Ala Met Val Asn Leu His Thr Ser Ala Gly Leu Ser Asn Gly Met
 65 70 75 80
 Ser Asn Ile Leu Thr Ala Tyr Met Asn Arg Thr Pro Leu Ile Ile Thr
 85 90 95
 Ala Gly Asn Gln Thr Arg Glu Met Leu Leu Met Glu Pro Trp Leu Thr
 100 105 110
 Asn Ile Glu Pro Glu Asn Leu Pro Lys Pro Trp Val Lys Trp Ser Tyr
 115 120 125
 Gln Pro Ala Arg Ala Glu Asp Val Pro Ala Ala Phe Met Arg Ala Tyr
 130 135 140
 Ala Met Ala Leu Gln Pro Pro Ala Gly Pro Val Phe Leu Ser Ile Pro
 145 150 155 160
 Leu Asp Asp Trp Asp Lys Pro Ala Glu Lys Asp Ala Ala Val Val Arg
 165 170 175
 Thr Val Ser Glu Arg Ile Gly Tyr Asp Pro Ile Arg Leu Lys Ser Phe

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180	185	190
Ala Asp Val Leu Ser Gln Ala Lys Asn Pro Val Leu Ile Tyr Gly Ser		
195	200	205
Ala Ile Ala Arg Gly Gln Gly Trp Asp Ala Gly Ile Ala Leu Ala Glu		
210	215	220
Lys Leu Asn Ile Pro Val Trp Ala Ala Pro Ala Ser Glu Arg Pro Pro		
225	230	235
Phe Pro Glu Thr His Pro Leu Tyr Ala Gly Gly Leu Pro Phe Ala Ile		
245	250	255
Gln Pro Leu Ala Asp Lys Leu Lys Gly His Asp Leu Ala Leu Ile Ile		
260	265	270
Gly Ala Pro Val Phe Arg Tyr Tyr Pro Tyr Val Ala Gly Glu Tyr Leu		
275	280	285
Pro Asp Gly Leu Arg Leu Leu His Ile Thr Asp Asp Pro Ile Glu Val		
290	295	300
Gly Arg Ala Pro Val Gly Asp Ser Met Leu Ser Asp Ala Val Leu Ala		
305	310	315
Val Glu Gly Leu Thr Gln Leu Val Ser Ala Arg Ala Ala Ser Gln Ala		
325	330	335
Lys Val Val Lys Gln Pro His Gly Met Ala Pro Tyr Pro Ala Ala Pro		
340	345	350
Glu Thr Val Asn Asn Ala Thr Thr Leu Ser Ala Ala Gln Leu Phe Arg		
355	360	365
Ala Leu Arg Glu Val Ser Pro Lys Glu Thr Val Leu Val Glu Glu Ser		
370	375	380
Pro Ser Asn Leu Gly Glu Leu His Arg Glu Trp Pro Ile Glu His Pro		
385	390	395
Asp Ser Phe Tyr Thr Phe Ala Ser Gly Ser Leu Gly Trp Asn Leu Pro		
405	410	415
Ala Ser Val Gly Ile Ala Leu Ala Glu Arg Asp Ser Gly Arg Asn Arg		
420	425	430
Pro Val Leu Ser Ile Ile Gly Asp Gly Ser Met Gln Tyr Ser Ile Gln		
435	440	445
Gly Leu Trp Ser Ala Ala Gln His Asn Leu Pro Ile Val Phe Val Ile		
450	455	460
Pro Arg Asn Ser Glu Tyr Ala Ile Leu Lys Ser Phe Ala Val Leu Glu		
465	470	475
Glu Thr Pro Gly Val Pro Gly Leu Asp Ile Pro Asn Leu Asp Ile Val		
485	490	495
Ala Leu Gly Lys Gly Tyr Gly Cys Thr Ala Val Lys Ala Thr Thr Val		
500	505	510
Glu Glu Val Gln Gln Ala Cys Lys Glu Ala Tyr Lys Arg Gln Gly Pro		
515	520	525
Thr Val Ile Glu Val Pro Ile Leu Pro Gln Ile Pro Pro Leu Ile		
530	535	540

<210> SEQ_ID NO 40

<211> LENGTH: 545

<212> TYPE: PRT

<213> ORGANISM: Acidobacterium capsulatum

<400> SEQUENCE: 40

Met Ser Ala Gly Asn Ala Phe Thr Val Trp Glu Ala Thr Tyr Asp Leu		
1	5	10
		15

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Leu Arg Lys Leu Gly Leu Thr Thr Val Phe Gly Asn Pro Gly Ser Thr
 20 25 30
 Glu Gln Pro Phe Leu Lys Asn Phe Pro Ser Asp Phe Asp Tyr Ile Leu
 35 40 45
 Ala Leu Gln Glu Ala Ser Ala Val Ala Met Ala Asp Gly Phe Ala Gln
 50 55 60
 Ala Thr Gly Ser Pro Ala Leu Val Asn Leu His Thr Asn Ala Gly Thr
 65 70 75 80
 Gly Asn Gly Met Gly Ser Ile Met Thr Ala Phe Gln Asn Lys Thr Pro
 85 90 95
 Leu Ile Ile Thr Ala Gly Gln Gln Thr Arg Glu Met Ile Ile Cys Asp
 100 105 110
 Pro Leu Leu Thr Asn Arg Asp Glu Thr Met Leu Pro Arg Pro Tyr Val
 115 120 125
 Lys Trp Ala Tyr Glu Pro Lys Arg Ala Gln Asp Val Pro Arg Ala Ile
 130 135 140
 Met Arg Ala Tyr Ala Leu Ala Leu Gln Pro Pro Ala Gly Pro Val Phe
 145 150 155 160
 Leu Ser Ile Pro Leu Asp Asp Trp Asp Gln Pro Ala Leu Gly Ile Ala
 165 170 175
 Asp Val Arg Thr Val Ser Ser Arg Val Ala Pro Asp Pro Asp Arg Ile
 180 185 190
 Arg Glu Phe Ala Ser Arg Ile Ser Gly Ala Lys Lys Pro Ala Leu Ile
 195 200 205
 Tyr Gly Pro Glu Ile Glu Lys Ala Gly Gly Trp Glu Ala Gly Ile Ala
 210 215 220
 Leu Ala Glu Lys Leu Arg Ala Pro Val Phe Arg Ala Pro Ala Ser Glu
 225 230 235 240
 Arg Met Ser Ile Ser Glu Thr His Pro Leu Phe Gln Met Gln Leu Pro
 245 250 255
 Gln Ala Met Gly Pro Ile Ser Thr Ile Leu Ala Gly Tyr Asp Leu Ile
 260 265 270
 Val Val Ile Gly Ala Pro Val Phe Arg Tyr Tyr Pro Tyr Val Pro Gly
 275 280 285
 Pro Val Val Pro Ala Gly Ala Glu Leu Leu Gln Ile Thr Asn Asp Pro
 290 295 300
 Thr Asp Ala Gly Ser Ala Leu Ile Gly Asp Ser Leu Leu Ser Asp Ala
 305 310 315 320
 Lys Leu Ala Leu Leu Ala Leu His Asp Leu Val Glu Asp Arg Ser Ser
 325 330 335
 Leu Pro Leu Pro Ala Arg Arg Glu Lys Lys Thr Pro Pro Ala Ser Ser
 340 345 350
 Thr Gly Met Pro Leu Thr Ala Glu Glu Leu Tyr Ala Ala Leu Gly Glu
 355 360 365
 Val Arg Pro Glu Asp Ala Ile Val Val Glu Glu Ser Pro Ser Asn Phe
 370 375 380
 Met Gln Phe Arg Asp Tyr Trp Pro Ala Leu Lys Pro Met Arg Tyr Phe
 385 390 395 400
 Thr Tyr Ala Ser Gly Gly Leu Gly His Asn Ala Pro Ser Ser Val Gly
 405 410 415
 Val Ala Leu Ala Gln Lys Lys Leu Gly Thr Gly Leu Pro Val Val Met
 420 425 430
 Leu Ile Gly Asp Gly Ser Leu Gln Tyr Ser Val Gln Ser Leu Ala Ser

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435 440 445

Ala Ala Gln His Asn Leu Lys Ile Ile Tyr Ile Val Pro Cys Asn Arg
 450 455 460

Glu Tyr Ala Ile Leu Lys Glu Phe Ala Val Leu Glu Arg Thr Pro Asn
 465 470 475 480

Val Pro Ala Leu Asp Leu Pro Tyr Leu Asp Ile Val Ser Leu Ala Gln
 485 490 495

Gly Tyr Gly Val Arg Gly Ile Lys Ala Asp Thr Lys Glu Gln Ile Gln
 500 505 510

Ala Ala Phe Arg Gln Ala Leu Ala Ala Glu Gly Pro Thr Leu Ile Ala
 515 520 525

Val Pro Ile Lys Gln Glu Leu Lys Pro Leu Ile Pro Pro Ser Val Lys
 530 535 540

Ala
 545

<210> SEQ ID NO: 41

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Desulfovibrio magneticus

<400> SEQUENCE: 41

Met Pro Thr Val Arg Asp Val Thr Phe Ala Leu Leu Arg Arg Leu Gly
 1 5 10 15

Leu Thr Thr Val Val Gly Asn Pro Gly Ser Thr Glu Glu Thr Phe Leu
 20 25 30

Lys Asn Phe Pro Asp Asp Phe Thr Tyr Ile Leu Ala Leu Gln Glu Ser
 35 40 45

Ser Val Val Gly Ile Ala Asp Gly Leu Ala Gln Gly Leu Gly Lys Pro
 50 55 60

Val Leu Val Asn Val His Thr Gly Ala Gly Met Gly Asn Ala Met Gly
 65 70 75 80

Cys Ile Leu Thr Ala Tyr Leu Asn Lys Thr Pro Leu Ile Ile Thr Ala
 85 90 95

Gly Gln Gln Thr Arg Asp Met Leu Leu Gly Glu Pro Phe Leu Thr Asn
 100 105 110

Ile Asp Glu Thr Met Leu Pro Lys Pro Trp Val Lys Trp Ser Tyr Glu
 115 120 125

Pro Lys Arg Pro Gln Asp Val Pro Gly Ala Phe Met Arg Ala Tyr Ala
 130 135 140

Met Ala Met Gln Gln Pro Gln Gly Pro Val Phe Leu Ser Leu Pro Leu
 145 150 155 160

Asp Asp Trp Glu Lys Asp Met Asp Ala Val Asp Val Tyr Arg Thr Val
 165 170 175

Ser Val Arg His Ala Pro Asp Pro Ala Arg Ile Ala Glu Phe Ala Ala
 180 185 190

Arg Ile Asn Ala Ser Ala Asn Pro Val Leu Val Tyr Gly Ala Asp Leu
 195 200 205

Ser Arg Ser Gln Ala Trp Glu Gln Gly Ile Ala Leu Ala Glu Ala Val
 210 215 220

Gln Ala Pro Val Trp Leu Gly Pro Phe Thr Glu Arg Val Pro Phe Pro
 225 230 235 240

His Asn His Pro Leu Tyr Ala Gly Val Leu Pro Pro Ala Val Gly Pro
 245 250 255

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Leu Ser Lys Ala Leu Ala Gly His Asp Leu Val Val Val Val Gly Ala
 260 265 270
 Pro Val Phe Arg Tyr Tyr Pro Trp Val Ala Gly Glu Thr Leu Pro Ala
 275 280 285
 Gly Ala Lys Leu Leu Gln Ile Ile Asp Asp Pro Tyr Glu Ala Gly Lys
 290 295 300
 Ala Val Val Gly Asp Ser Leu Val Ala Asp Ser Leu Leu Ala Val Glu
 305 310 315 320
 Ala Leu Leu Pro Leu Val Ala Lys Arg Pro Ala Arg Gly Pro Val Arg
 325 330 335
 Pro Glu Arg Ala Lys Val Ala Val Pro Asp Asp Ala Pro Leu Pro Leu
 340 345 350
 Thr Pro Arg Gln Ile Phe Gly Val Leu Ser Glu Val Ile Val Gly Gly
 355 360 365
 Asp Cys Ile Leu Val Asn Glu Ser Pro Ser Asn Met Ala Asp Leu Ala
 370 375 380
 Ala Thr Pro Leu Gly Val Val Thr Gln Pro Asp Ser Ser Phe Val Met
 385 390 395 400
 Ala Ser Gly Gly Leu Gly Trp Gly Met Pro Ala Ala Val Gly Leu Ala
 405 410 415
 Leu Ala Glu Lys Ala Ser Gly Arg Gly Lys Pro Val Val Ala Val Ile
 420 425 430
 Gly Asp Gly Ser Phe Gln Tyr Ser Leu Gln Ser Ile Trp Thr Gly Val
 435 440 445
 Gln His Gly Ala His Val Val Tyr Val Val Leu Arg Asn Asp Glu Tyr
 450 455 460
 Gly Ile Leu Lys Ser Phe Ala Arg Leu Glu Glu Thr Pro Gly Val Pro
 465 470 475 480
 Gly Leu Asp Leu Pro Gly Leu Asp Ile Val Ser Leu Gly Lys Gly Tyr
 485 490 495
 Gly Ala Ala Thr Ala Lys Val Asp Thr Pro Ala Ala Ile Arg Glu Ala
 500 505 510
 Phe Ala Asp Ala Leu Ala Phe Lys Gly Val Ser Val Ile Glu Ile Ala
 515 520 525
 Ala Asp Lys His Val Gly Asp Leu Ile Pro Lys
 530 535

<210> SEQ ID NO 42
 <211> LENGTH: 536
 <212> TYPE: PRT
 <213> ORGANISM: Burkholderia multivorans

<400> SEQUENCE: 42

Met Ser Gly Gln Pro His Ala Ala Ala Thr Pro Ala Thr Thr Val Arg
 1 5 10 15
 Asp Ala Val Ile His Leu Phe Arg Gln Phe Gly Ile Asp Arg Val Phe
 20 25 30
 Gly Asn Pro Gly Ser Thr Glu Leu Pro Met Phe Arg Asp Phe Pro Asp
 35 40 45
 Asp Phe Arg Tyr Val Leu Gly Leu Gln Glu Ala Val Val Val Gly Met
 50 55 60
 Ala Asp Gly Tyr Ala Gln Ala Ser Gly Asn Ala Ala Val Val Asn Leu
 65 70 75 80
 His Ser Ala Ala Gly Val Gly Asn Ala Met Gly Asn Leu Phe Thr Ala
 85 90 95

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Tyr Lys Asn Arg Thr Pro Leu Ile Val Thr Ala Gly Gln Gln Ala Arg
100 105 110

Ala Ile Leu Pro Phe Glu Pro Phe Leu Gly Ala Ala Gln Ala Thr Glu
115 120 125

Leu Pro Lys Pro Tyr Val Lys Trp Ser Ile Glu Pro Ala Arg Ala Gln
130 135 140

Asp Val Pro Ala Ala Ile Ala Arg Ala Tyr Arg Ile Ala Met Gln Glu
145 150 155 160

Pro Arg Gly Pro Val Phe Val Ser Ile Pro Val Asp Asp Trp Asp Gln
165 170 175

Pro Ala Glu Leu Leu Pro Pro Arg Asp Val Ser Gln Val Val Arg Pro
180 185 190

Asp Pro Asp Ala Leu Ala Arg Leu Gly Asp Ala Leu Asp Ala Ala Gln
195 200 205

Arg Pro Ala Phe Val Val Gly Ala Ala Leu Asp Arg Ala Gly Ala Trp
210 215 220

Asp Glu Ala Val Arg Leu Ala Glu Arg His Arg Ala Arg Val Tyr Val
225 230 235 240

Ala Pro Met Ser Gly Arg Cys Ser Phe Pro Glu Asp His Pro Leu Phe
245 250 255

Ala Gly Phe Leu Pro Ala Ile Arg Glu Gln Ile Val Ala Arg Leu Asp
260 265 270

Gly His Asp Leu Val Phe Ala Phe Gly Ala Pro Ala Phe Thr Tyr His
275 280 285

Ile Glu Gly Phe Gly Pro His Val Pro Pro Gly Ala Thr Leu Val Gln
290 295 300

Leu Val Asp Asp Pro Gly Thr Ala Ala Trp Thr Pro Gln Gly Asp Ala
305 310 315 320

Val Val Gly Asn Leu Lys Leu Ala Ala Arg Asp Leu Leu Ala Arg Pro
325 330 335

Ala Pro Ala Glu Arg Pro Met Pro Ala Ala Arg Ala Pro Arg Gln Arg
340 345 350

Val Ala Pro Pro Val Ala Gly Glu Arg Met Ser Ala Ala Phe Ala Leu
355 360 365

Gln Thr Leu Ala Asp Leu Arg Asp Val His Asp Ile Val Val Glu Glu
370 375 380

Ala Pro Ser Ala Arg Pro Ile Met Gln Glu His Leu Pro Phe Thr Arg
385 390 395 400

Ser Gly Thr Phe Tyr Thr Met Asp Ser Gly Gly Leu Gly Tyr Gly Met
405 410 415

Pro Ala Ala Val Gly Val Ala Leu Ala Gln Pro Glu Arg Arg Val Ile
420 425 430

Ala Leu Ile Gly Asp Gly Ser Ser Leu Tyr Ser Ile Gln Ala Leu Trp
435 440 445

Ser Ala Ala Gln Leu Gly Leu Pro Ile Thr Phe Val Ile Leu Asn Asn
450 455 460

Arg Arg Tyr Ala Ala Leu Gln Asp Phe Ala Pro Val Phe Gly Phe Gly
465 470 475 480

Pro Asp Asp Pro Val Gln Gly Thr Asp Leu Pro Asp Leu Asp Phe Val
485 490 495

Ala Leu Ala Ala Gly Phe Gly Cys Arg Gly Val Arg Val Gly Asp Pro
500 505 510

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Ala Arg Leu Arg Asp Thr Leu Ala Asp Ala Leu Arg Ala Thr Ala Pro
515 520 525

Val Val Val Asp Val Glu Ile Ala
530 535

<210> SEQ ID NO 43
<211> LENGTH: 536
<212> TYPE: PRT
<213> ORGANISM: Burkholderia multivorans

<400> SEQUENCE: 43

Met Ser Gly Gln Pro His Ala Ala Ala Thr Pro Ala Thr Thr Val Arg
1 5 10 15

Asp Ala Val Ile His Leu Phe Arg Gln Phe Gly Ile Asp Arg Val Phe
20 25 30

Gly Asn Pro Gly Ser Thr Glu Leu Pro Met Phe Arg Asp Phe Pro Asp
35 40 45

Asp Phe Arg Tyr Val Leu Gly Leu Gln Glu Ala Val Val Val Gly Met
50 55 60

Ala Asp Gly Tyr Ala Gln Ala Ser Gly Asn Ala Ala Val Val Asn Leu
65 70 75 80

His Ser Ala Ala Gly Val Gly Asn Ala Met Gly Asn Leu Phe Thr Ala
85 90 95

Tyr Lys Asn Arg Thr Pro Leu Ile Val Thr Ala Gly Gln Gln Ala Arg
100 105 110

Ala Ile Leu Pro Phe Glu Pro Phe Leu Gly Ala Ala Gln Ala Thr Glu
115 120 125

Leu Pro Lys Pro Tyr Val Lys Trp Ser Ile Glu Pro Ala Arg Ala Gln
130 135 140

Asp Val Pro Ala Ala Ile Ala Arg Ala Tyr Arg Ile Ala Met Gln Glu
145 150 155 160

Pro Arg Gly Pro Val Phe Val Ser Ile Pro Val Asp Asp Trp Asp Gln
165 170 175

Pro Ala Glu Leu Leu Pro Ala Arg Glu Val Ser Gln Val Val Arg Pro
180 185 190

Asp Pro Asp Ala Leu Val Arg Leu Gly Asp Ala Leu Asn Ala Ala Gln
195 200 205

Arg Pro Ala Phe Val Val Gly Ala Ala Ile Asp Arg Ala Gly Ala Trp
210 215 220

Asp Glu Ala Val Arg Leu Ala Glu Arg His Arg Ala Arg Val Tyr Val
225 230 235 240

Ala Pro Met Ser Gly Arg Cys Ser Phe Pro Glu Asp His Pro Leu Phe
245 250 255

Ala Gly Phe Leu Pro Ala Ile Arg Glu Lys Ile Val Ala Arg Leu Asp
260 265 270

Gly His Asp Leu Val Phe Ala Phe Gly Ala Pro Ala Phe Thr Tyr His
275 280 285

Ile Glu Gly Phe Gly Pro His Val Pro Pro Gly Ala Thr Leu Leu Gln
290 295 300

Leu Val Asp Asp Pro Gly Thr Ala Ala Trp Thr Pro Gln Gly Asp Ala
305 310 315 320

Val Val Gly Asn Leu Lys Leu Ala Ala Arg Asp Leu Leu Ala Arg Pro
325 330 335

Ala Pro Ala Glu Arg Pro Met Pro Ala Ala Arg Ala Pro Arg Glu Arg
340 345 350

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Ile Ala Pro Pro Ala Gly Glu Arg Met Ser Ala Ala Phe Val Leu
 355 360 365

Gln Thr Leu Ala Asp Leu Arg Asp Ala His Asp Ile Val Val Glu Glu
 370 375 380

Ala Pro Ser Ala Arg Pro Ile Met Gln Ala His Leu Pro Phe Thr Arg
 385 390 395 400

Ser Gly Thr Phe Tyr Thr Met Asp Ser Gly Gly Leu Gly Tyr Gly Met
 405 410 415

Pro Ala Ala Val Gly Val Ala Leu Ala Gln Pro Gly Arg Arg Val Ile
 420 425 430

Gly Leu Ile Gly Asp Gly Ser Ser Leu Tyr Ser Ile Gln Ala Leu Trp
 435 440 445

Ser Ala Ala Gln Leu Arg Leu Pro Ile Thr Phe Val Ile Leu Asn Asn
 450 455 460

Arg Arg Tyr Ala Ala Leu Gln Asp Phe Ala Pro Val Phe Gly Phe Gly
 465 470 475 480

Pro Asp Asp Pro Val Gln Gly Thr Asp Leu Pro Asp Leu Asp Phe Val
 485 490 495

Ala Leu Ala Ala Ala Phe Gly Cys Arg Gly Val Arg Val Asp Asp Pro
 500 505 510

Ala Arg Leu Arg Asp Thr Leu Ala Asp Ala Leu Arg Ala Thr Ala Pro
 515 520 525

Val Val Val Asp Val Asp Ile Ala
 530 535

<210> SEQ ID NO 44

<211> LENGTH: 536

<212> TYPE: PRT

<213> ORGANISM: Burkholderia multivorans

<400> SEQUENCE: 44

Met Ser Gly Gln Pro His Ala Ala Ala Thr Pro Ala Thr Thr Val Arg
 1 5 10 15

Asp Ala Val Ile His Leu Phe Arg Gln Phe Gly Ile Asp Arg Val Phe
 20 25 30

Gly Asn Pro Gly Ser Thr Glu Leu Pro Met Phe Arg Asp Phe Pro Asp
 35 40 45

Asp Phe Arg Tyr Val Leu Gly Leu Gln Glu Ala Val Val Val Gly Met
 50 55 60

Ala Asp Gly Tyr Ala Gln Ala Ser Gly Asn Ala Ala Val Val Asn Leu
 65 70 75 80

His Ser Ala Ala Gly Val Gly Asn Ala Met Gly Asn Leu Phe Thr Ala
 85 90 95

Tyr Lys Asn Arg Thr Pro Leu Ile Val Thr Ala Gly Gln Gln Ala Arg
 100 105 110

Ala Ile Leu Pro Phe Glu Pro Phe Leu Gly Ala Ala Gln Ala Thr Glu
 115 120 125

Leu Pro Lys Pro Tyr Val Lys Trp Ser Ile Glu Pro Ala Arg Ala Gln
 130 135 140

Asp Val Pro Ala Ala Ile Ala Arg Ala Tyr Arg Ile Ala Met Gln Glu
 145 150 155 160

Pro Arg Gly Pro Val Phe Val Ser Ile Pro Val Asp Asp Trp Asp Gln
 165 170 175

Pro Ala Glu Leu Leu Pro Ala Arg Glu Val Ser Gln Val Val Arg Pro

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180	185	190	
Asp Pro Asp Ala Leu Ala Arg	Leu Gly Asp Ala Leu Asp Ala Ala Gln		
195	200	205	
Arg Pro Ala Phe Val Val	Gly Ala Ala Ile Asp Arg Ala Gly Ala Trp		
210	215	220	
Asp Glu Ala Val Arg Leu Ala Glu Arg His	Arg Ala Arg Val Tyr Val		
225	230	235	240
Ala Pro Met Ser Gly Arg Cys Ser Phe Pro	Glu Asp His Pro Leu Phe		
245	250	255	
Ala Gly Phe Leu Pro Ala Ile Arg	Glu Lys Ile Val Ala Arg Leu Asp		
260	265	270	
Gly His Asp Leu Val Phe Ala Phe Gly	Ala Pro Ala Phe Thr Tyr His		
275	280	285	
Ile Glu Gly Phe Gly Pro His	Val Pro Pro Gly Ala Thr Leu Val Gln		
290	295	300	
Leu Val Asp Asp Pro Gly Thr Ala Ala Trp	Thr Pro Gln Gly Asp Ala		
305	310	315	320
Val Val Gly Asn Leu Lys Leu Ala Ala Arg	Asp Leu Leu Ala Arg Pro		
325	330	335	
Ala Pro Ala Glu Arg Pro Met Pro	Ala Ala Arg Ala Pro Arg Glu Arg		
340	345	350	
Val Ala Pro Pro Ala Ala Gly	Glu Arg Met Ser Ala Ala Phe Val Leu		
355	360	365	
Gln Thr Leu Ala Asp Leu Arg	Asp Ala His Asp Ile Val Val Glu Glu		
370	375	380	
Ala Pro Ser Ala Arg Pro Ile Met Gln	Ala His Leu Pro Phe Thr Gln		
385	390	395	400
Ser Gly Thr Phe Tyr Thr Met Asp Ser	Gly Gly Leu Gly Tyr Gly Met		
405	410	415	
Pro Ala Ala Val Gly Val Ala Leu Ala Gln	Pro Gly Arg Arg Val Ile		
420	425	430	
Gly Leu Ile Gly Asp Gly Ser Ser	Leu Tyr Ser Ile Gln Ala Leu Trp		
435	440	445	
Ser Ala Ala Gln Leu Arg Leu Pro Ile	Thr Phe Val Ile Leu Asn Asn		
450	455	460	
Arg Arg Tyr Ala Ala Leu Gln Asp Phe	Ala Pro Val Phe Gly Phe Gly		
465	470	475	480
Pro Asp Asp Pro Val Gln Gly Thr Asp	Leu Pro Asp Leu Asp Phe Val		
485	490	495	
Ala Leu Ala Ala Ala Phe Gly Cys Arg	Gly Val Arg Val Asp Asp His		
500	505	510	
Ala Arg Leu Arg Asp Thr Leu Ala Asp	Ala Leu Arg Ala Thr Ala Pro		
515	520	525	
Val Val Val Asp Val Glu Ile Ala			
530	535		

<210> SEQ_ID NO 45
<211> LENGTH: 540
<212> TYPE: PRT
<213> ORGANISM: Bradyrhizobium sp.

<400> SEQUENCE: 45

Met Ala Lys Thr Thr Lys Thr Thr Lys	Pro Val Thr Val Lys Gln		
1	5	10	15

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Ala Thr Phe Glu Leu Leu Arg Ala Phe Gly Ile Lys Lys Val Phe Gly
 20 25 30

Asn Pro Gly Ser Thr Glu Leu Pro Phe Leu Ser Asp Trp Pro Asp Asp
 35 40 45

Ile Asp Tyr Val Leu Gly Leu Gln Glu Ala Ser Val Val Gly Met Ala
 50 55 60

Asp Gly Tyr Ala Gln Ala Thr Arg Asn Ala Gly Phe Val Asn Leu His
 65 70 75 80

Ser Ala Ala Gly Val Gly Asn Ala Leu Gly Asn Ile Tyr Thr Ala His
 85 90 95

Arg Asn Gln Thr Pro Leu Val Ile Thr Ala Gly Gln Gln Ala Arg Ala
 100 105 110

Ile Leu Pro Leu Gln Ala Phe Leu Tyr Ala Glu Arg Ala Ser Glu Phe
 115 120 125

Pro Arg Pro Tyr Val Lys Tyr Ser Val Glu Pro Ala Arg Pro Glu Asp
 130 135 140

Val Pro Gly Ala Ile Ala Arg Ala Tyr Tyr Thr Ala Met Gln Pro Pro
 145 150 155 160

Cys Gly Pro Thr Phe Val Ser Ile Pro Ile Asp Asp Trp Met His Pro
 165 170 175

Ala Gln Pro Val Ser Ala Arg Lys Val Ser Arg Glu Leu Gly Pro Asp
 180 185 190

Arg Ala Ala Met Asp Glu Leu Val Ala Ala Leu Thr Ala Ala Arg Asn
 195 200 205

Pro Ala Leu Val Val Gly Pro Gly Val Asp Arg Ala Gly Cys Val Thr
 210 215 220

Leu Met Val Gln Leu Ala Glu Arg Ala Lys Ala Gly Val Trp Val Ser
 225 230 235 240

Pro Phe Ser Ala Arg Cys Ser Phe Pro Glu Arg His Pro Leu Phe Gln
 245 250 255

Gly Phe Leu His Ala Ser Pro Gly Gln Leu Ser Asp Ala Leu Lys Pro
 260 265 270

His Asp Leu Val Leu Val Ile Gly Ala Pro Val Phe Thr Phe His Val
 275 280 285

Glu Gly His Ala Ala Ile Phe Asp Gly Ala Thr Ala Ile Tyr Gln Ile
 290 295 300

Thr Asp Asp Ala Asp Gly Ala Ala Val Pro Pro Ile Ser Thr Ser Ile
 305 310 315 320

Ile Ala Thr Met Arg Pro Ala Leu Leu Leu Leu Glu Leu Leu Pro
 325 330 335

Glu Thr Lys Arg Ala Ala Pro Gln Ala Arg Val Leu Pro Glu Ala Pro
 340 345 350

Lys Pro Ser Asp Pro Ile Pro Val Asp Tyr Leu Leu His Thr Leu Gly
 355 360 365

Gln Ala Leu Pro Ala Gly Ala Ala Leu Val Glu Glu Ile Pro Ser His
 370 375 380

Arg Pro Leu Met His Lys Phe Met Pro Met Pro Gly Ala Asp Ser Phe
 385 390 395 400

Tyr Thr Met Ser Ser Gly Gly Leu Gly Tyr Ser Leu Pro Ala Ala Val
 405 410 415

Gly Met Ala Leu Gly Arg Pro Lys Asp Arg Ile Val Cys Leu Ile Gly
 420 425 430

Asp Gly Ser Ala Met Tyr Ser Leu Gln Ala Leu Trp Thr Ala Ala Gln

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435	440	445
Arg Arg Leu Pro Met Thr Val Val Ile Asn Asn Ser Gly Tyr Gly		
450	455	460
Ala Met Arg Ser Phe Ser Gln Val Met Gln Val Arg Asn Val Pro Gly		
465	470	475
Leu Glu Leu Pro Gly Leu Asp Phe Val Lys Leu Ala Glu Gly Met Gly		
485	490	495
Cys Glu Ala Val Arg Val Ser Arg Ser Ala Glu Leu Pro Ala Ala Leu		
500	505	510
Ala Arg Gly Leu Ala His Asp Gly Pro Ser Leu Val Glu Val Met Val		
515	520	525
Asp Ser Ala Val Pro Leu Leu Tyr Ala Gln Lys Ser		
530	535	540

<210> SEQ_ID NO 46

<211> LENGTH: 540

<212> TYPE: PRT

<213> ORGANISM: Bradyrhizobium japonicum

<400> SEQUENCE: 46

Met Ser Lys Asn Gly Lys Thr Gly Ser Lys Ser Val Thr Val Lys Gln		
1	5	10
Ala Thr Ile Asp Leu Leu Arg Ala Phe Gly Ile Asp Arg Val Phe Gly		
20	25	30
Asn Pro Gly Ser Thr Glu Leu Pro Phe Leu Ser Asp Trp Pro Asp Asp		
35	40	45
Ile Asp Tyr Val Leu Ala Leu Gln Glu Ala Ser Ala Val Gly Met Ala		
50	55	60
Asp Gly Tyr Ala Gln Ala Thr Arg Asn Ala Gly Phe Val Asn Leu His		
65	70	75
Ser Ala Ala Gly Val Gly Asn Ala Leu Gly Asn Ile Tyr Thr Ala His		
85	90	95
Arg Asn Gln Thr Pro Leu Val Ile Thr Ala Gly Gln Gln Ala Arg Ser		
100	105	110
Ile Leu Pro Leu Gln Ala Phe Leu Tyr Ala Glu Arg Ala Ser Glu Phe		
115	120	125
Pro Arg Pro Tyr Val Lys Tyr Ser Val Glu Pro Ala Arg Pro Glu Asp		
130	135	140
Val Pro Ala Ala Ile Ala Arg Ala Tyr Tyr Thr Ala Met Gln Pro Pro		
145	150	155
Cys Gly Pro Thr Phe Val Ser Ile Pro Ile Asp Asp Trp Thr His Ala		
165	170	175
Thr Ala Pro Val Glu Ala Arg Lys Val Ser Arg Glu Ile Gly Pro Glu		
180	185	190
Arg Glu Ala Met Lys Ala Leu Val Ala Ala Phe Gly Ser Ala Lys His		
195	200	205
Pro Ala Leu Val Val Gly Pro Gly Val Asp Arg Ala Gly Ala Val Asp		
210	215	220
Leu Met Val Arg Val Ala Glu Lys Ala Lys Ala Ser Val Trp Val Ser		
225	230	235
Pro Phe Ser Ala Arg Cys Ser Phe Pro Glu Arg His Pro Gln Phe Ala		
245	250	255
Gly Phe Leu His Ala Ser Pro Ala Gln Leu Ser Asp Ala Leu Arg Glu		
260	265	270

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His Asp Leu Val Val Val Val Gly Ala Pro Val Phe Thr Phe His Val
 275 280 285
 Glu Gly His Ala Ala Ile Phe Asp Gly Gly Ala Thr Ile Phe Gln Ile
 290 295 300
 Thr Asp Asp Pro Asp Ala Ala Ala Val Thr Pro Val Gly Thr Ser Ile
 305 310 315 320
 Val Ala Thr Met Lys Pro Ala Leu Ser Leu Leu Leu Asp Leu Leu Pro
 325 330 335
 Glu Ser Lys Arg Ala Thr Pro Lys Gly Arg Thr Leu Pro Pro Ala Pro
 340 345 350
 Gln Ala Ala Asp Pro Leu Pro Val Glu Phe Leu Leu His Ser Leu Ala
 355 360 365
 Gln Ala Met Pro Asp Gly Thr Ser Leu Val Glu Glu Val Pro Ser His
 370 375 380
 Arg Pro Ala Met Gln Lys Phe Met Pro Met Leu Gly Gln Asp Ser Phe
 385 390 395 400
 Tyr Thr Met Ser Ser Gly Gly Leu Gly Tyr Ser Leu Pro Ala Ala Val
 405 410 415
 Gly Met Ala Leu Gly Lys Pro Lys Ser Arg Thr Val Cys Leu Ile Gly
 420 425 430
 Asp Gly Ser Ala Met Tyr Ser Ile Gln Ala Leu Trp Thr Ala Ala Gln
 435 440 445
 Arg Lys Leu Pro Leu Thr Val Val Val Ile Asn Asn Ser Gly Tyr Gly
 450 455 460
 Ala Met Arg Ser Phe Ser Gln Val Met Gln Val Arg Asn Val Pro Gly
 465 470 475 480
 Leu Glu Leu Pro Gly Ile Asp Phe Val Arg Leu Ala Glu Gly Met Gly
 485 490 495
 Cys His Ala Val Arg Val Ser Arg Ala Ala Glu Leu Gly Glu Thr Leu
 500 505 510
 Lys Arg Gly Met Ala Phe Glu Gly Thr Ser Leu Val Glu Val Ile Val
 515 520 525
 Asp Ser Ala Val Pro Val Leu Tyr Gly Gln Lys His
 530 535 540

<210> SEQ ID NO 47

<211> LENGTH: 534

<212> TYPE: PRT

<213> ORGANISM: Burkholderia cenocepacia

<400> SEQUENCE: 47

Met Ser Gly His Pro Pro Pro Ser Ala Ser Ile Thr Val Arg Asp Ala
 1 5 10 15
 Val Val Asp Leu Leu Arg Gln Phe Gly Ile Asp Arg Val Phe Gly Asn
 20 25 30
 Pro Gly Ser Thr Glu Leu Pro Met Phe Arg Asp Phe Pro Asp Asp Phe
 35 40 45
 Arg Tyr Val Leu Gly Leu His Glu Ala Val Val Val Gly Met Ala Asp
 50 55 60
 Gly His Ala Gln Ala Thr Gly Asn Ala Ala Val Val Asn Leu His Ser
 65 70 75 80
 Ala Ala Gly Val Gly Asn Ala Met Gly Asn Leu Phe Thr Ala Phe Lys
 85 90 95
 Asn Arg Thr Pro Leu Ile Val Thr Ala Gly Gln Gln Ala Arg Ala Ile
 100 105 110

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Leu Pro Phe Asp Pro Phe Leu Gly Ala Thr Gln Ala Ala Glu Leu Pro
 115 120 125
 Lys Pro Tyr Val Lys Trp Ser Ile Glu Pro Ala Arg Ala Gln Asp Val
 130 135 140
 Pro Ala Ala Ile Ala Arg Ala Tyr Arg Ile Ala Met Gln Glu Pro Arg
 145 150 155 160
 Gly Pro Val Phe Val Ser Ile Pro Val Asp Asp Trp Asp Gln Pro Ala
 165 170 175
 Glu Arg Leu Pro Arg Arg Asp Val Ser Ser Ile Val Arg Pro Asp Pro
 180 185 190
 Asp Ala Leu Ala Arg Leu Gly Asp Ala Leu Asp Ala Ala Arg Arg Pro
 195 200 205
 Ala Phe Val Val Gly Ala Ala Val Asp Arg Ala Gly Ala Trp Asp Asp
 210 215 220
 Val Val Arg Leu Ala Glu Arg His Arg Ala Arg Val Tyr Val Ala Pro
 225 230 235 240
 Met Ser Gly Arg Cys Ser Phe Pro Glu Asp His Pro Leu Phe Ala Gly
 245 250 255
 Phe Leu Pro Ala Ile Arg Glu Lys Ile Ile Ala Arg Leu Asp Gly His
 260 265 270
 Asp Leu Val Phe Ala Phe Gly Ala Pro Ala Phe Thr Tyr His Ile Glu
 275 280 285
 Gly Phe Gly Pro His Val Pro Pro Gly Ala Thr Leu Val Gln Leu Val
 290 295 300
 Asp Asp Pro Gly Val Ala Ala Trp Thr Pro Ser Gly Asp Ala Val Val
 305 310 315 320
 Gly Asn Leu Arg Leu Ala Ala Arg Asp Leu Leu Ala Arg Pro Ala Pro
 325 330 335
 Pro Glu Arg Pro Met Pro Ala Ala Arg Ala Pro Arg Val Arg Val Asp
 340 345 350
 Ala Pro Ala Ala Gly Glu Arg Met Ser Val Ala Phe Ala Leu Gln Thr
 355 360 365
 Leu Ala Asp Val Arg Asp Ala Ser Asp Ile Val Val Glu Glu Ala Pro
 370 375 380
 Ser Ala Arg Pro Val Met Gln Glu His Leu Pro Phe Thr Arg Ser Gly
 385 390 395 400
 Thr Phe Tyr Thr Met Asp Ser Gly Gly Leu Gly Tyr Gly Met Pro Ala
 405 410 415
 Ala Val Gly Val Ala Leu Ala Gln Pro Gly Arg Arg Val Ile Gly Leu
 420 425 430
 Ile Gly Asp Gly Ser Ser Leu Tyr Ser Ile Gln Ala Leu Trp Ser Ala
 435 440 445
 Ala Gln Leu Lys Leu Pro Ile Thr Phe Val Ile Leu Asn Asn Arg Arg
 450 455 460
 Tyr Ala Ala Leu Gln Asp Phe Ala Pro Val Phe Gly Phe Gly Pro Gly
 465 470 475 480
 Asp Pro Val Gln Gly Thr Glu Leu Pro Asp Leu Asp Phe Val Ala Leu
 485 490 495
 Ala Gln Gly Met Gly Cys Arg Gly Val Arg Val Ala Glu Ala Ala Lys
 500 505 510
 Leu Arg Asp Thr Leu Thr Asp Ala Leu Arg Ala Ala Thr Pro Val Val
 515 520 525

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Val Glu Val Glu Ile Ala
530

<210> SEQ ID NO 48

<211> LENGTH: 555

<212> TYPE: PRT

<213> ORGANISM: *Burkholderia cenocepacia*

<400> SEQUENCE: 48

Met	Asn	Gly	Leu	Arg	Phe	Asp	Thr	Val	Glu	Thr	Ala	Lys	Pro	Ser	Arg
1				5					10					15	

Arg Arg Pro Ser Met Ser Gly Thr Pro Ser Gln Ser Ala Ala Pro Val
20 25 30

Thr Val Arg Asp Ala Val Ile Asp Leu Phe Arg Gln Phe Gly Ile Asp
35 40 45

Arg Val Phe Gly Asn Pro Gly Ser Thr Glu Leu Pro Met Phe Arg Asp
50 55 60

Phe	Pro	Ala	Asp	Phe	Arg	Tyr	Val	Leu	Gly	Leu	Gln	Glu	Ala	Val	Val
65				70				75						80	

Val Gly Met Ala Asp Gly His Ala Gln Ala Thr Gly Asn Ala Ala Val
85 90 95

Val Asn Leu His Ser Ala Ala Gly Val Gly Asn Ala Met Gly Asn Leu
100 105 110

Phe Thr Ala Phe Lys Asn Arg Ser Pro Leu Ile Val Thr Ala Gly Gln
115 120 125

130 135 140

145 150 155 160

165 170 175

180 185 190

195	200	205
Val Arg Pro Asp Pro Asp Ala Leu Ala Arg Leu Gly Asp Val Leu Asp		

Ala Ala Arg Arg Pro Ala Phe Val Val Gly Ala Ala Val Asp Arg Ala

Gly Ala Trp Asp Asp Val Val Arg Leu Ala Glu Arg His Arg Ala Arg

Val Tyr Val Ala Pro Met Ser Gly Arg Cys Ser Phe Pro Glu Asp His

Pro Leu Phe Ala Gly Phe Leu Pro Ala Ile Arg Glu Lys Ile Val Ala
 275 280 285

Arg Leu Asp Gly His Asp Leu Val Phe Ala Phe Gly Ala Pro Ala Phe
290 295 300

Thr Tyr His Ile Glu Gly Phe Gly Pro His Val Pro Pro Gly Ala Thr
305 310 315 320

Leu Val Gln Leu Val Asp Asp Pro Gly Val Ala Ala Trp Thr Pro Ser
 325 330 335

Gly Asp Ala Val Val Gly Asn Val Arg Leu Ala Ala Arg Asp Leu Leu
340 345 350

Ala Arg Pro Ala Pro Pro Glu Arg Pro Met Pro Ala Pro Arg Ala Pro
355 360 365

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Arg Leu Arg Val Asp Ala Pro Ala Ala Gly Glu Arg Met Ser Val Ala
 370 375 380
 Phe Ala Leu Gln Thr Leu Ala Asp Val Arg Asp Ala His Asp Ile Val
 385 390 395 400
 Val Glu Glu Ala Pro Ser Ala Arg Pro Val Met Gln Glu His Leu Pro
 405 410 415
 Phe Thr Arg Ser Gly Thr Phe Tyr Thr Met Asp Ser Gly Gly Leu Gly
 420 425 430
 Tyr Gly Met Pro Ala Ala Val Gly Val Ala Leu Ala Gln Pro Gly Arg
 435 440 445
 Arg Val Ile Ala Leu Ile Gly Asp Gly Ser Ser Leu Tyr Ser Ile Gln
 450 455 460
 Ala Leu Trp Ser Ala Ala Gln Leu Lys Leu Pro Ile Thr Phe Val Ile
 465 470 475 480
 Leu Asn Asn Arg Arg Tyr Ala Ala Leu Gln Asp Phe Ala Pro Val Phe
 485 490 495
 Gly Phe Gly Pro Gly Asp Pro Val Gln Gly Thr Asp Leu Pro Asp Leu
 500 505 510
 Asp Phe Val Ala Leu Ala Gln Gly Met Gly Cys Arg Gly Val Arg Val
 515 520 525
 Ala Glu Ala Ala Lys Leu Arg Asp Ala Leu Thr Asp Ala Leu Arg Ala
 530 535 540
 Ala Thr Pro Val Ile Val Glu Val Glu Ile Ala
 545 550 555

<210> SEQ ID NO 49
 <211> LENGTH: 535
 <212> TYPE: PRT
 <213> ORGANISM: Burkholderia cenocepacia
 <400> SEQUENCE: 49

Met	Ser	Gly	Thr	Pro	Ser	Gln	Ser	Ala	Ala	Pro	Val	Thr	Val	Arg	Asp
1								5			10			15	

Ala Val Ile Asp Leu Phe Arg Gln Phe Gly Ile Asp Arg Val Phe Gly
 20 25 30

Asn	Pro	Gly	Ser	Thr	Glu	Leu	Pro	Met	Phe	Arg	Asp	Phe	Pro	Ala	Asp
35								35	40		45				

Phe Arg Tyr Val Leu Gly Leu Gln Glu Ala Val Val Val Gly Met Ala
 50 55 60

Asp	Gly	His	Ala	Gln	Ala	Thr	Gly	Asn	Ala	Ala	Val	Val	Asn	Leu	His
65								65	70		75			80	

Ser Ala Ala Gly Val Gly Asn Ala Met Gly Asn Leu Phe Thr Ala Phe
 85 90 95

Lys	Asn	Arg	Ser	Pro	Leu	Ile	Val	Thr	Ala	Gly	Gln	Gln	Ala	Arg	Ala
								100	105		110				

Ile Leu Pro Phe Asp Pro Phe Leu Gly Ala Thr Gln Ala Ala Glu Leu
 115 120 125

Pro	Lys	Pro	Tyr	Val	Lys	Trp	Ser	Ile	Glu	Pro	Ala	Arg	Ala	Gln	Asp
130								130	135		140				

Val Pro Ala Ala Ile Ala Arg Ala Tyr Arg Ile Ala Met Gln Glu Pro
 145 150 155 160

Arg	Gly	Pro	Val	Phe	Val	Ser	Ile	Pro	Val	Asp	Asp	Trp	Asp	Gln	Pro
								165	170		175				

Ala Glu Leu Leu Pro Arg Arg Asp Val Ser Ser Ile Val Arg Pro Asp

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180	185	190
Pro Asp Ala Leu Ala Arg Leu Gly Asp Ala Leu Asp Ala Ala Arg Arg		
195	200	205
Pro Ala Phe Val Val Gly Ala Ala Val Asp Arg Ala Gly Ala Trp Asp		
210	215	220
Asp Val Val Arg Val Ala Glu Arg His Arg Ala Arg Val Tyr Val Ala		
225	230	235
Pro Met Ser Gly Arg Cys Ser Phe Pro Glu Asp His Pro Leu Phe Ala		
245	250	255
Gly Phe Leu Pro Ala Ile Arg Glu Lys Ile Val Ala Arg Leu Asp Gly		
260	265	270
His Asp Leu Val Phe Ala Phe Gly Ala Pro Ala Phe Thr Tyr His Ile		
275	280	285
Glu Gly Phe Gly Pro His Val Pro Pro Gly Ala Thr Leu Val Gln Leu		
290	295	300
Val Asp Asp Pro Gly Val Ala Ala Trp Thr Pro Ser Gly Asp Ala Val		
305	310	315
320		
Val Gly Asn Leu Arg Leu Ala Ala Arg Asp Leu Leu Ala Arg Pro Ala		
325	330	335
Pro Pro Glu Arg Pro Met Pro Ala Pro Arg Ala Pro Arg Leu Arg Val		
340	345	350
Asp Ala Pro Ala Ala Gly Glu Arg Met Ser Val Ala Phe Ala Leu Gln		
355	360	365
Thr Leu Ala Asp Val Arg Asp Ala His Asp Ile Val Val Glu Ala		
370	375	380
Pro Ser Ala Arg Pro Val Met Gln Glu His Leu Pro Phe Thr Arg Ser		
385	390	395
400		
Gly Thr Phe Tyr Thr Met Asp Ser Gly Gly Leu Gly Tyr Gly Met Pro		
405	410	415
Ala Ala Val Gly Val Ala Leu Ala Gln Pro Gly Arg Arg Val Ile Ala		
420	425	430
Leu Ile Gly Asp Gly Ser Ser Leu Tyr Ser Ile Gln Ala Leu Trp Ser		
435	440	445
Ala Ala Gln Leu Lys Leu Pro Ile Thr Phe Val Ile Leu Asn Asn Arg		
450	455	460
Arg Tyr Ala Ala Leu Gln Asp Phe Ala Pro Val Phe Gly Phe Gly Pro		
465	470	475
480		
Gly Asp Pro Val Gln Gly Thr Asp Leu Pro Asp Leu Asp Phe Val Ala		
485	490	495
Leu Ala Gln Gly Met Gly Cys Arg Gly Val Arg Val Ala Glu Ala Ala		
500	505	510
Arg Leu Arg Asp Ala Leu Thr Asp Ala Leu Arg Ala Ala Thr Pro Val		
515	520	525
Val Val Glu Val Glu Ile Ala		
530	535	

<210> SEQ_ID NO 50

<211> LENGTH: 535

<212> TYPE: PRT

<213> ORGANISM: Burkholderia cenocepacia

<400> SEQUENCE: 50

Met Ser Gly Thr Pro Ser Gln Ser Ala Ala Pro Val Thr Val Arg Asp		
1	5	10
		15

-continued

Ala Val Ile Asp Leu Phe Arg Gln Phe Gly Ile Asp Arg Val Phe Gly
20 25 30

Asn Pro Gly Ser Thr Glu Leu Pro Met Phe Arg Asp Phe Pro Ala Asp
35 40 45

Phe Arg Tyr Val Leu Gly Leu Gln Glu Ala Val Val Val Gly Met Ala
50 55 60

Asp Gly His Ala Gln Ala Thr Gly Asn Ala Ala Val Val Asn Leu His
65 70 75 80

Ser Ala Ala Gly Val Gly Asn Ala Met Gly Asn Leu Phe Thr Ala Phe
85 90 95

Lys Asn Arg Thr Pro Leu Ile Val Thr Ala Gly Gln Gln Ala Arg Ala
100 105 110

Ile Leu Pro Phe Asp Pro Phe Leu Gly Ala Thr Gln Ala Ala Glu Leu
115 120 125

Pro Lys Pro Tyr Val Lys Trp Ser Ile Glu Pro Ala Arg Ala Gln Asp
130 135 140

Val Pro Ala Ala Ile Ala Arg Ala Tyr Arg Ile Ala Met Gln Glu Pro
145 150 155 160

Arg Gly Pro Val Phe Val Ser Ile Pro Val Asp Asp Trp Asp Gln Pro
165 170 175

Ala Glu Leu Leu Pro Arg Arg Asp Val Ser Ser Ile Val Arg Pro Asp
180 185 190

Pro Asp Ala Leu Ala Arg Leu Gly Asp Ala Leu Asp Ala Ala Arg Arg
195 200 205

Pro Ala Phe Val Val Gly Ala Ala Val Asp Arg Ala Gly Ala Trp Asp
210 215 220

Asp Val Val Arg Leu Ala Glu Arg His Arg Ala Arg Val Tyr Val Ala
225 230 235 240

Pro Met Ser Gly Arg Cys Ser Phe Pro Glu Asp His Pro Leu Phe Ala
245 250 255

Gly Phe Leu Pro Ala Ile Arg Glu Lys Ile Val Ala Arg Leu Asp Gly
260 265 270

His Asp Leu Val Phe Ala Phe Gly Ala Pro Ala Phe Thr Tyr His Ile
275 280 285

Glu Gly Phe Gly Pro His Val Pro Pro Gly Ala Thr Leu Val Gln Leu
290 295 300

Val Asp Asp Pro Gly Val Ala Ala Trp Thr Pro Ser Gly Asp Ala Val
305 310 315 320

Val Gly Asn Leu Arg Leu Ala Ala Arg Asp Leu Leu Ala Arg Pro Ala
325 330 335

Pro Pro Glu Arg Pro Met Pro Ala Pro Arg Ala Pro Arg Leu Arg Val
340 345 350

Asp Ala Pro Ala Ala Gly Glu Arg Met Ser Val Ala Phe Ala Leu Gln
355 360 365

Thr Leu Ala Asp Val Arg Asp Ala His Asp Ile Val Val Glu Ala
370 375 380

Pro Ser Ala Arg Pro Val Met Gln Glu His Leu Pro Phe Thr Arg Ser
385 390 395 400

Gly Thr Phe Tyr Thr Met Asp Ser Gly Gly Leu Gly Tyr Gly Met Pro
405 410 415

Ala Ala Val Gly Val Ala Phe Ala Gln Pro Gly Arg Arg Val Ile Ala
420 425 430

Leu Ile Gly Asp Gly Ser Ser Leu Tyr Ser Ile Gln Ala Leu Trp Ser

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435 440 445

Ala Ala Gln Leu Lys Leu Pro Ile Thr Phe Val Ile Leu Asn Asn Arg
450 455 460

Arg Tyr Ala Ala Leu Gln Asp Phe Ala Pro Val Phe Gly Phe Gly Pro
465 470 475 480

Gly Asp Pro Val Gln Gly Thr Asp Leu Pro Asp Leu Asp Phe Val Ala
485 490 495

Leu Ala Gln Gly Met Gly Cys Arg Gly Val Arg Val Ala Glu Ala Ala
500 505 510

Arg Leu Arg Asp Ala Leu Thr Asp Ala Leu Arg Ala Ala Thr Pro Val
515 520 525

Val Val Glu Val Glu Ile Ala
530 535

<210> SEQ_ID NO 51

<211> LENGTH: 542

<212> TYPE: PRT

<213> ORGANISM: Bradyrhizobium japonicum

<400> SEQUENCE: 51

Met Ala Thr Gly Thr Asp Thr Phe Glu Gln Arg Arg Val Thr Ala Pro
1 5 10 15

Thr Val Arg Asp Ala Val Val Asp Leu Leu Arg Arg Leu Asn Met Thr
20 25 30

Ser Val Phe Ala Asn Pro Gly Ser Thr Glu Leu Pro Leu Phe Arg Asn
35 40 45

Phe Pro Asp Asp Phe Arg Tyr Val Leu Gly Leu Gln Glu Ala Val Val
50 55 60

Val Gly Met Ala Asp Gly Phe Ala Gln Ala Thr Arg Asn Ala Ala Phe
65 70 75 80

Val Asn Leu His Ser Ala Ala Gly Val Gly Asn Ala Met Gly Asn Ile
85 90 95

Phe Thr Ala Phe Lys Asn Arg Thr Pro Leu Val Ile Thr Ala Gly Gln
100 105 110

Gln Ala Arg Ser Ile Leu Pro Phe Asp Pro Phe Leu Ala Ser Arg Glu
115 120 125

Ala Thr Glu Leu Pro Lys Pro Tyr Val Lys Trp Ser Ile Glu Pro Ala
130 135 140

Arg Ala Glu Asp Val Pro His Ala Ile Ala Arg Ala Tyr Tyr Ile Ala
145 150 155 160

Met Thr Gln Pro Cys Gly Pro Val Leu Val Ser Val Pro Val Asp Asp
165 170 175

Trp Asp Arg Pro Ala Glu Tyr Leu Pro Thr Arg Thr Val Ser Gln Gln
180 185 190

Val Arg Pro Asp Pro Ala Ile Leu Asp Gln Ile Gly Ser Ala Leu Asp
195 200 205

Arg Ser Lys Arg Pro Ala Phe Val Val Gly Ala Ala Ala Asp Arg Asp
210 215 220

Gly Ala Phe Asn Glu Val Arg Gln Leu Ala Glu Ala His Asn Ala Arg
225 230 235 240

Val Phe Thr Ala Pro Met Ser Gly Arg Cys Ser Phe Pro Glu Asp His
245 250 255

Arg Leu Phe Ala Gly Phe Leu Pro Ala Ile Arg Glu Lys Ile Val Arg
260 265 270

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Leu Leu Asp Gly His Asp Leu Val Phe Ala Ile Gly Ala Pro Ala Phe
 275 280 285
 Ser Tyr His Val Glu Gly Phe Gly Pro His Leu Pro Asp Gly Ala Glu
 290 295 300
 Leu Phe Gln Leu Thr Asp Asp Pro Gln Thr Ala Ala Trp Thr Pro Glu
 305 310 315 320
 Gly Met Ala Ala Val Gly Ser Val Arg Leu Gly Leu Leu Asp Leu Leu
 325 330 335
 Ala Arg Ala Thr Pro Pro Ile Arg Val Thr Pro Pro Ala Arg Thr Ile
 340 345 350
 Ala Arg Arg Val Glu Pro Thr Thr Pro Leu Ser Thr Ala Phe Val Met
 355 360 365
 Gln Thr Ile Ala Asp Met Lys Pro Ala Asp Gly Ile Ile Val Glu Glu
 370 375 380
 Ala Pro Gly Ala Arg Ser Val Met Gln Ala His Leu Pro Ile Thr Gln
 385 390 395 400
 Ser Glu Ala Phe Tyr Thr Met Asp Ser Gly Gly Leu Gly Tyr Gly Met
 405 410 415
 Pro Ala Ala Val Gly Val Ala Leu Gly Lys Pro Gly Arg Pro Val Ile
 420 425 430
 Ala Leu Met Gly Asp Gly Ser Ser Leu Tyr Ser Ile Gln Ala Ile Trp
 435 440 445
 Ser Ala Ala Gln Leu Ser Leu Pro Val Thr Phe Val Ile Leu Lys Asn
 450 455 460
 Gly Arg Tyr Ala Ala Leu Gln Asp Phe Ala Pro Val Phe Gly Phe Gly
 465 470 475 480
 Ser Gln Glu His Val Gln Gly Thr Asp Leu Pro Gly Leu Asp Phe Val
 485 490 495
 Ser Ile Ala Arg Gly Leu Gly Cys Ser Ala Ile His Val Glu Thr Ala
 500 505 510
 Lys Gly Leu His Asp Ala Leu Val Lys Ala Phe Ser Ser Lys Arg Pro
 515 520 525
 Thr Leu Val Glu Val Glu Val Glu Asp Arg Asp Leu Gln Lys
 530 535 540

<210> SEQ ID NO 52
 <211> LENGTH: 542
 <212> TYPE: PRT
 <213> ORGANISM: Rhodopseudomonas palustris
 <400> SEQUENCE: 52

Met	Pro	Ala	Lys	Lys	Ser	Lys	Gln	Pro	Ser	Ala	Ala	Val	Thr	Thr	Val
1								5		10			15		

Lys Ser Ala Thr Leu Asp Leu Leu Arg Ala Phe Lys Ile Asp Lys Val
 20 25 30

Phe Gly Asn Pro Gly Ser Thr Glu Leu Pro Phe Leu Ser Asp Trp Pro
 35 40 45

Asp Asp Ile Asp Tyr Val Leu Ala Leu Gln Glu Ala Ser Ala Val Ala
 50 55 60

Met Ala Asp Gly Tyr Ala Gln Ala Thr Arg Asn Ala Gly Phe Val Asn
 65 70 75 80

Leu His Ser Ala Ala Gly Val Gly Asn Ala Leu Gly Asn Ile Tyr Ser
 85 90 95

Ala Phe Lys Asn Gln Thr Pro Leu Val Ile Thr Ala Gly Gln Gln Ala
 100 105 110

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Arg Ser Leu Leu Pro Leu Gln Ala Phe Leu Gly Ala Glu Arg Ala Ser
 115 120 125
 Glu Phe Pro Arg Pro Tyr Val Lys Tyr Ser Val Glu Pro Ala Arg Ala
 130 135 140
 Glu Asp Val Pro Ala Ala Ile Ala Arg Ala Tyr Tyr Val Ala Met Gln
 145 150 155 160
 Pro Pro Cys Gly Pro Thr Phe Val Ser Val Pro Ile Asp Asp Trp Ala
 165 170 175
 Arg Pro Ala Ala Pro Val Pro Pro Arg Thr Ile Thr Arg Glu Ile Gly
 180 185 190
 Pro Asp Arg Ser Ala Met Gln Val Leu Ala Asp Thr Leu Ala Asn Ala
 195 200 205
 Lys Lys Pro Ala Leu Val Val Gly Pro Ala Ile Asp Arg Ala Ala Ala
 210 215 220
 Val Gly Leu Met Ala Arg Leu Ala Glu Arg Ala Lys Ala Pro Val Trp
 225 230 235 240
 Val Ser Pro Phe Ser Ala Arg Cys Ser Phe Pro Glu Arg His Pro Leu
 245 250 255
 Phe Ala Gly Phe Leu Pro Ala Ser Pro Gly Gln Leu Ser Glu Thr Leu
 260 265 270
 Gly Ala Tyr Asp Val Ile Val Leu Ile Gly Ala Pro Val Phe Thr Phe
 275 280 285
 His Val Glu Gly His Ala Ala Ile Phe Asp Gly Ala Ser Gln Leu Phe
 290 295 300
 Gln Ile Thr Asp Asp Ala Glu Ala Ala Ser Val Thr Pro Leu Gly Ala
 305 310 315 320
 Ser Ile Ile Ala Thr Met Thr Pro Ala Leu Thr Leu Leu Glu Leu
 325 330 335
 Leu Pro Glu Thr Lys Arg Ala Ala Pro Pro Ala Arg Ala Val Pro Pro
 340 345 350
 Ala Pro Arg Pro Ala Glu Pro Met Pro Val Glu Tyr Leu Leu His Thr
 355 360 365
 Leu Arg Ala Ala Met Pro Glu Ser Ala Met Leu Val Glu Glu Ala Pro
 370 375 380
 Ser His Arg Pro Ala Met Gln Thr Tyr Met Pro Met Pro Gly Gln Asp
 385 390 395 400
 Ser Phe Ala Thr Met Ala Ser Gly Gly Leu Gly Trp Ser Leu Pro Ala
 405 410 415
 Ser Val Gly Phe Ala Leu Ala His Pro Asn Arg Arg Thr Val Cys Leu
 420 425 430
 Ile Gly Asp Gly Ser Ala Met Tyr Ser Ile Gln Ala Leu Trp Thr Ala
 435 440 445
 Ala Gln Arg Lys Leu Pro Leu Thr Val Val Leu Asn Asn Gly Gly
 450 455 460
 Tyr Gly Ala Met Arg Ser Phe Ser Gln Val Met Gln Val Arg Asn Val
 465 470 475 480
 Pro Gly Leu Glu Leu Pro Gly Ile Asp Phe Thr Ala Leu Ala Gln Ser
 485 490 495
 Leu Gly Cys Asp Ala Val Arg Val Thr Arg Ser Glu Glu Leu Ala Pro
 500 505 510
 Ala Leu Thr Arg Ala Leu Ala Trp Asp Gly Val Ser Leu Val Glu Val
 515 520 525

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Met	Leu	Asp	Thr	Ser	Val	Pro	Met	Leu	Tyr	Ala	Arg	Asn	Gly
530						535						540	

<210> SEQ ID NO 53

<211> LENGTH: 535

<212> TYPE: PRT

<213> ORGANISM: Burkholderia sp.

<400> SEQUENCE: 53

Met	Ser	Gly	Tyr	Gln	Pro	Pro	Ser	Ala	Ala	Pro	Ile	Thr	Val	Arg	Asp
1					5			10			15				

Ala	Val	Ile	Asp	Leu	Leu	Arg	Gln	Phe	Gly	Ile	Asp	Arg	Val	Phe	Gly
		20			25					30					

Asn	Pro	Gly	Ser	Thr	Glu	Leu	Pro	Met	Phe	Arg	Asp	Phe	Pro	Asp	Asp
					35		40		45						

Phe	Arg	Tyr	Val	Leu	Gly	Leu	His	Glu	Ala	Val	Val	Gly	Met	Ala
			50		55			60						

Asp	Gly	His	Ala	Gln	Ala	Thr	Gly	Asn	Ala	Ala	Val	Val	Asn	Leu	His
65						70		75			80				

Ser	Ala	Ala	Gly	Val	Gly	Asn	Ala	Met	Gly	Asn	Leu	Phe	Thr	Ala	Phe
			85		90			95							

Lys	Asn	Arg	Thr	Pro	Leu	Ile	Val	Thr	Ala	Gly	Gln	Gln	Ala	Arg	Ala
					100		105		110						

Ile	Leu	Pro	Phe	Asp	Pro	Phe	Leu	Gly	Ala	Thr	Gln	Ala	Ala	Glu	Leu
		115			120			125							

Pro	Lys	Pro	Tyr	Val	Lys	Trp	Ser	Ile	Glu	Pro	Ala	Arg	Ala	Gln	Asp
					130		135		140						

Val	Pro	Ala	Ala	Ile	Ala	Arg	Ala	Tyr	Arg	Ile	Ala	Met	Gln	Glu	Pro
145					150		155		160						

Arg	Gly	Pro	Val	Phe	Val	Ser	Ile	Pro	Val	Asp	Asp	Trp	Asp	Gln	Pro
			165		170		175								

Ala	Glu	Leu	Leu	Pro	Arg	Arg	Asp	Val	Ser	Ser	Val	Val	Arg	Pro	Asp
			180		185		190								

Pro	Asp	Ala	Leu	Ala	Arg	Leu	Gly	Asp	Thr	Leu	Asp	Ala	Ala	Arg	Arg
			195		200		205								

Pro	Ala	Phe	Val	Val	Gly	Ala	Ala	Val	Asp	Arg	Ala	Gly	Ala	Trp	Asp
		210		215		220									

Asp	Val	Val	Arg	Leu	Ala	Glu	Arg	Ala	Arg	Val	Tyr	Val	Ala		
225				230		235		240							

Pro	Met	Ser	Gly	Arg	Cys	Ser	Phe	Pro	Glu	Asp	His	Pro	Leu	Phe	Ala
				245		250		255							

Gly	Phe	Leu	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Val	Ala	Arg	Leu	Asp	Gly
		260			265		270								

His	Asp	Leu	Val	Phe	Ala	Phe	Gly	Ala	Pro	Ala	Phe	Thr	Tyr	His	Ile
		275		280		285									

Glu	Gly	Phe	Gly	Pro	His	Val	Pro	Pro	Gly	Ala	Thr	Leu	Val	Gln	Leu
		290		295		300									

Val	Asp	Asp	Pro	Gly	Ile	Ala	Ala	Trp	Thr	Pro	Ser	Gly	Asp	Ala	Val
305				310		315		320							

Val	Gly	Asn	Leu	Arg	Leu	Ala	Ala	Arg	Asp	Leu	Leu	Ala	Arg	Pro	Ala
			325		330		335								

Pro	Pro	Glu	Arg	Pro	Met	Pro	Ala	Pro	Arg	Pro	Pro	Arg	Ala	Arg	Val
			340		345		350								

Glu	Pro	Pro	Ala	Ala	Gly	Glu	Arg	Met	Ser	Val	Ala	Phe	Ala	Leu	Gln
			355		360		365								

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Thr Leu Ala Asp Val Arg Asp Ala His Asp Ile Val Val Glu Glu Ala
 370 375 380
 Pro Ser Ala Arg Ala Val Met Gln Glu His Leu Pro Phe Thr His Ser
 385 390 395 400
 Gly Thr Phe Tyr Thr Met Asp Ser Gly Gly Leu Gly Tyr Gly Met Pro
 405 410 415
 Ala Ala Val Gly Val Ala Leu Ala His Pro Gly Arg Arg Val Ile Gly
 420 425 430
 Leu Ile Gly Asp Gly Ser Ser Leu Tyr Ser Ile Gln Ala Leu Trp Ser
 435 440 445
 Ala Ala Gln Leu Lys Leu Pro Ile Thr Phe Val Ile Leu Asn Asn Arg
 450 455 460
 Arg Tyr Ala Ala Leu Gln Asp Phe Ala Pro Val Phe Gly Phe Gly Pro
 465 470 475 480
 Asp Asp Pro Val Gln Gly Thr Asp Leu Pro Asn Leu Asp Phe Val Ala
 485 490 495
 Leu Ala Gln Gly Met Gly Cys Arg Gly Val Arg Val Thr Asp Ala Ala
 500 505 510
 His Leu Arg Asp Thr Leu Thr Glu Ala Leu Arg Ala Ala Thr Pro Val
 515 520 525
 Val Val Glu Val Glu Ile Ala
 530 535

<210> SEQ_ID NO 54
 <211> LENGTH: 548
 <212> TYPE: PRT
 <213> ORGANISM: Delftia acidovorans

<400> SEQUENCE: 54

Met Gln Ala Pro Thr Thr Pro Arg Ser Gln Pro Ala Glu Ala Ser Ser
 1 5 10 15
 Ser Thr Ala Thr Ser Thr Ala Thr Tyr Thr Val Arg His Ala Val Ile
 20 25 30
 Ala Met Leu Arg Glu Leu Gly Met Thr Arg Ile Phe Gly Asn Pro Gly
 35 40 45
 Ser Thr Glu Leu Pro Leu Phe Arg Asp Tyr Pro Glu Asp Phe Ser Tyr
 50 55 60
 Val Leu Gly Leu Gln Glu Thr Val Val Val Gly Met Ala Asp Gly His
 65 70 75 80
 Ala Gln Ala Thr Arg Asn Ala Ser Phe Val Asn Leu His Ser Ala Ala
 85 90 95
 Gly Val Gly His Ala Met Ala Asn Ile Phe Thr Ala Phe Lys Asn Arg
 100 105 110
 Thr Pro Leu Val Ile Thr Ala Gly Gln Gln Ala Arg Ser Leu Leu Gln
 115 120 125
 Phe Asp Pro Phe Leu His Ser Ser Gln Ala Ala Glu Leu Pro Lys Pro
 130 135 140
 Tyr Val Lys Trp Ser Cys Glu Pro Ala Arg Ala Glu Asp Val Pro Gln
 145 150 155 160
 Ala Leu Ala Arg Ala Tyr Tyr Ile Ala Met Gln Glu Pro Arg Gly Pro
 165 170 175
 Val Leu Val Ser Ile Pro Ala Asp Asp Trp Asp Lys Pro Ala Glu Pro
 180 185 190
 Val Thr Leu Arg His Val Gly Phe Glu Thr Arg Pro Asp Pro Arg Thr

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195 200 205

Leu Asp Leu Ile Gly Gln Ala Leu Asp Ala Ala Arg Ala Pro Ala Leu
 210 215 220

Val Val Gly Ala Ala Val Asp Arg Ala Gln Gly Trp Asp Ala Val Val
 225 230 235 240

Ala Leu Ala Glu Arg His Gln Ala Arg Val Phe Val Ala Pro Met Ser
 245 250 255

Gly Arg Cys Ser Phe Pro Glu Asp His Pro Leu Phe Ala Gly Phe Leu
 260 265 270

Pro Ala Met Arg Glu Arg Ile Val Gln Leu Leu Ser Gly His Asp Val
 275 280 285

Val Phe Ala Val Gly Ala Ala Ala Phe Thr Tyr His Val Glu Gly Glu
 290 295 300

Gly Pro His Ile Pro Glu Gly Thr Ala Leu Tyr Gln Leu Ile Glu Asp
 305 310 315 320

Pro Ala Ile Ala Ala Trp Ala Pro Val Gly Thr Ala Ala Val Gly Asn
 325 330 335

Val Arg Met Gly Val Glu Glu Leu Leu Gln Arg Pro Ala Pro Ala Pro
 340 345 350

Arg Gln Ala Pro Ala Pro Arg Pro Ala Ala Pro Val Pro Ala Ala Pro
 355 360 365

Ala Ala Gly Asp Arg Met Ser Val Ala Phe Ala Met His Thr Leu Ala
 370 375 380

Gln Val Arg Asp Arg His Ser Ile Val Val Glu Glu Ala Pro Ser Ser
 385 390 395 400

Arg Ser Thr Ile Gln Thr Tyr Leu Pro Ile Phe His Ser Gly Thr Phe
 405 410 415

Tyr Thr Met Cys Ser Gly Leu Gly His Ser Met Pro Ala Ala Val
 420 425 430

Gly Val Ala Leu Ala Lys Pro Glu Ala Lys Val Val Ala Val Ile Gly
 435 440 445

Asp Gly Ser Ala Met Tyr Ala Ile Gln Ala Leu Trp Ser Ala Ala Gln
 450 455 460

Leu Arg Leu Pro Ile Ser Phe Val Ile Leu Lys Asn Arg Arg Tyr Ala
 465 470 475 480

Ala Leu Gln Asp Phe Ala His Val Phe Gly Tyr Arg Glu Gly Glu Lys
 485 490 495

Val Glu Gly Thr Glu Leu Pro Asp Ile Asp Phe Val Ala Leu Ala Arg
 500 505 510

Gly Gln Gly Cys Asp Gly Val His Val Glu Asn Ala Ala Glu Leu Ala
 515 520 525

Asp Val Leu Glu Arg Ala Leu Ala His Pro Lys Pro Ile Val Val Glu
 530 535 540

Val Glu Val Ala
 545

<210> SEQ_ID NO 55

<211> LENGTH: 560

<212> TYPE: PRT

<213> ORGANISM: Bradyrhizobium sp.

<400> SEQUENCE: 55

Met Pro Gly Thr Leu Asp Cys Phe Val Ala Ser Leu Leu Ala Met Thr
 1 5 10 15

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Ala Ile Arg Gly Thr Pro Leu Ala Lys Lys Thr Thr Thr Lys Pro Val
 20 25 30
 Thr Val Lys Gln Ala Thr Phe Asp Leu Leu Arg Ala Phe Gly Ile Lys
 35 40 45
 Lys Val Phe Gly Asn Pro Gly Ser Thr Glu Leu Pro Phe Leu Ser Asp
 50 55 60
 Trp Pro Asp Asp Ile Asp Tyr Val Leu Gly Leu Gln Glu Ala Ser Val
 65 70 75 80
 Val Gly Met Ala Asp Gly Tyr Ala Gln Ala Thr Arg Asn Ala Gly Phe
 85 90 95
 Val Asn Leu His Ser Ala Ala Gly Val Gly Asn Ala Leu Gly Asn Ile
 100 105 110
 Tyr Thr Ala His Arg Asn Gln Thr Pro Leu Val Ile Thr Ala Gly Gln
 115 120 125
 Gln Ala Arg Ser Ile Leu Pro Leu Gln Ala Phe Leu Tyr Ala Glu Arg
 130 135 140
 Pro Ser Glu Phe Pro Arg Pro Tyr Val Lys Tyr Ser Val Glu Pro Ala
 145 150 155 160
 Arg Pro Glu Asp Val Pro Gly Ala Ile Ala Arg Ala Tyr Tyr Thr Ala
 165 170 175
 Met Gln Pro Pro Cys Gly Pro Thr Phe Val Ser Ile Pro Ile Asp Asp
 180 185 190
 Trp Met His Pro Ala Gln Pro Val Ala Ala Arg Lys Val Ser Arg Glu
 195 200 205
 Leu Gly Pro Asp Arg Ala Ala Ile Glu Glu Leu Val Ala Ala Leu Gly
 210 215 220
 Ala Ala Lys Asn Pro Ala Leu Val Val Gly Pro Gly Ile Asp Arg Ala
 225 230 235 240
 Ala Cys Val Asp Leu Met Val Gln Val Ala Glu Lys Ala Lys Ala Gly
 245 250 255
 Val Trp Val Ser Pro Phe Ser Ala Arg Cys Ser Phe Pro Glu Arg His
 260 265 270
 Pro Gln Phe Gln Gly Phe Leu His Ala Ser Pro Gly Gln Leu Ser Glu
 275 280 285
 Ala Leu Lys Pro Tyr Asp Ile Val Val Ile Gly Ala Pro Val Phe
 290 295 300
 Thr Phe His Val Glu Gly His Ala Ala Ile Phe Asp Gly Ala Thr Thr
 305 310 315 320
 Leu Tyr Gln Ile Thr Asp Asp Ala Glu Gly Ala Ser Val Pro Pro Ile
 325 330 335
 Gly Thr Ser Ile Val Ala Thr Met Arg Pro Ala Leu Ser Leu Leu Arg
 340 345 350
 Glu Leu Leu Pro Glu Ser Gln Arg Ala Ala Pro Lys Gly Arg Val Met
 355 360 365
 Pro Glu Pro Pro Asp Ala Ser Asp Pro Ile Pro Val Asp Tyr Leu Leu
 370 375 380
 His Thr Leu Ser Gln Ala Leu Pro Pro Gly Ala Ala Ile Val Glu Glu
 385 390 395 400
 Ile Pro Ser His Arg Pro Val Met Tyr Lys Tyr Met Pro Met Pro Gly
 405 410 415
 Ala Asp Ser Phe Tyr Thr Met Ala Ser Gly Gly Leu Gly Tyr Ser Leu
 420 425 430
 Pro Ala Ser Val Gly Met Ala Leu Gly Arg Pro Asn Asp Arg Ile Val

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435 440 445

Cys Leu Ile Gly Asp Gly Ser Ala Met Tyr Ser Leu Gln Ala Leu Trp
450 455 460

Thr Ala Ala Gln Arg Lys Leu Arg Leu Thr Ile Val Val Ile Asn Asn
465 470 475 480

Ser Gly Tyr Gly Ala Met Arg Ser Phe Ser Gln Val Met Gln Val Arg
485 490 495

Asn Val Pro Gly Leu Glu Leu Pro Gly Leu Asp Phe Val Lys Leu Ala
500 505 510

Glu Gly Leu Gly Cys Asp Ala Val Arg Val Ser Arg Ser Ala Asp Leu
515 520 525

Pro Ala Ala Leu Ala Arg Gly Leu Ala His Asp Gly Thr Ser Leu Val
530 535 540

Glu Val Met Val Asp Ser Ala Val Pro Leu Leu Tyr Ala Gln Lys Arg
545 550 555 560

<210> SEQ ID NO 56

<211> LENGTH: 346

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 56

Met Gln Asn Ile Ile Arg Lys Gly Gly Thr Met Lys Ala Ala Val Val
1 5 10 15

Thr Lys Asp His His Val Asp Val Thr Asp Lys Thr Leu Arg Ser Leu
20 25 30

Lys His Gly Glu Ala Leu Leu Lys Met Glu Cys Cys Gly Val Cys His
35 40 45

Thr Asp Leu His Val Lys Asn Gly Asp Phe Gly Asp Lys Thr Gly Val
50 55 60

Ile Leu Gly His Glu Gly Ile Gly Val Val Ala Glu Val Gly Pro Gly
65 70 75 80

Val Thr Ser Leu Lys Pro Gly Asp Arg Ala Ser Val Ala Trp Phe Tyr
85 90 95

Glu Gly Cys Gly His Cys Glu Tyr Cys Asn Ser Gly Asn Glu Thr Leu
100 105 110

Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser Val Asp Gly Gly Met Ala
115 120 125

Glu Glu Cys Ile Val Val Ala Asp Tyr Ala Val Lys Val Pro Asp Gly
130 135 140

Leu Asp Ser Ala Ala Ala Ser Ser Ile Thr Cys Ala Gly Val Thr Thr
145 150 155 160

Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg Pro Gly Gln Trp Ile Ala
165 170 175

Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu Ala Leu Gln Tyr Ala Lys
180 185 190

Asn Val Phe Asn Ala Lys Val Ile Ala Ile Asp Val Asn Asp Glu Gln
195 200 205

Leu Lys Leu Ala Thr Glu Met Gly Ala Asp Leu Ala Ile Asn Ser Arg
210 215 220

Thr Glu Asp Ala Ala Lys Ile Val Gln Glu Lys Thr Gly Gly Ala His
225 230 235 240

Ala Ala Val Val Thr Ala Val Ala Lys Ala Ala Phe Asn Ser Ala Val
245 250 255

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Asp Ala Val Arg Ala Gly Gly Arg Val Val Ala Val Gly Leu Pro Pro
260 265 270

Glu Ser Met Ser Leu Asp Ile Pro Arg Leu Val Leu Asp Gly Ile Glu
275 280 285

Val Val Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Thr Glu Ala Phe
290 295 300

Gln Phe Ala Ala Glu Gly Lys Val Val Pro Lys Val Ala Leu Arg Pro
305 310 315 320

Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu Met Glu Glu Gly Lys Ile
325 330 335

Arg Gly Arg Met Val Ile Asp Phe Arg Arg
340 345

<210> SEQ_ID NO 57

<211> LENGTH: 346

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 57

Met Gln Asn Ile Ile Arg Lys Gly Gly Thr Met Lys Ala Ala Val Val
1 5 10 15

Thr Lys Asp His His Val Asp Val Thr Asp Lys Thr Leu Arg Ser Leu
20 25 30

Lys His Gly Glu Ala Leu Leu Lys Met Glu Cys Cys Gly Val Cys His
35 40 45

Thr Asp Leu His Val Lys Asn Gly Asp Phe Gly Asp Lys Thr Gly Val
50 55 60

Ile Leu Gly His Glu Gly Ile Gly Val Val Ala Glu Val Gly Pro Gly
65 70 75 80

Val Thr Ser Leu Lys Pro Gly Asp Arg Ala Ser Val Ala Trp Phe Tyr
85 90 95

Glu Gly Cys Gly His Cys Glu Tyr Cys Asn Ser Gly Asn Glu Thr Leu
100 105 110

Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser Val Asp Gly Gly Met Ala
115 120 125

Glu Glu Cys Ile Val Val Ala Asp Tyr Ala Val Lys Val Pro Asp Gly
130 135 140

Leu Asp Ser Ala Ala Ala Asn Ser Ile Thr Cys Ala Gly Val Thr Thr
145 150 155 160

Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg Pro Gly Gln Trp Ile Ala
165 170 175

Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu Ala Leu Gln Tyr Ala Lys
180 185 190

Asn Val Phe Asn Ala Lys Val Ile Ala Ile Asp Val Asn Asp Glu Gln
195 200 205

Leu Lys Leu Ala Thr Glu Met Gly Ala Asp Leu Ala Ile Asn Ser Arg
210 215 220

Thr Glu Asp Ala Ala Lys Ile Val Gln Glu Lys Thr Gly Gly Ala His
225 230 235 240

Ala Ala Val Val Thr Ala Val Ala Lys Ala Ala Phe Asn Ser Ala Val
245 250 255

Asp Ala Val Arg Ala Gly Gly Arg Val Val Ala Val Gly Leu Pro Pro
260 265 270

Glu Ser Met Ser Leu Asp Ile Pro Arg Leu Val Leu Asp Gly Ile Glu
275 280 285

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Val Val Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Thr Glu Ala Phe
290 295 300

Gln Phe Ala Ala Glu Gly Lys Val Val Pro Lys Val Ala Leu Arg Pro
305 310 315 320

Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu Met Glu Glu Gly Lys Ile
325 330 335

Arg Gly Arg Met Val Ile Asp Phe Arg Arg
340 345

<210> SEQ ID NO 58

<211> LENGTH: 346

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 58

Met Gln Asn Ile Ile Arg Lys Gly Gly Thr Met Lys Ala Ala Val Val
1 5 10 15

Thr Lys Asp His His Val Asp Val Thr Asp Lys Thr Leu Arg Ser Leu
20 25 30

Lys His Gly Glu Ala Leu Leu Lys Met Glu Cys Cys Gly Val Cys His
35 40 45

Thr Asp Leu His Val Lys Asn Gly Asp Phe Gly Asp Lys Thr Gly Val
50 55 60

Ile Leu Gly His Glu Gly Ile Gly Val Val Ala Glu Val Gly Pro Gly
65 70 75 80

Val Thr Ser Leu Lys Pro Gly Asp Arg Ala Ser Val Ala Trp Phe Tyr
85 90 95

Glu Gly Cys Gly His Cys Glu Tyr Cys Asn Ser Gly Asn Glu Thr Leu
100 105 110

Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser Val Asp Gly Gly Met Ala
115 120 125

Glu Glu Cys Ile Val Val Ala Asp Tyr Ala Val Lys Val Pro Asp Gly
130 135 140

Leu Asp Ser Ala Ala Ala Ser Ser Ile Thr Cys Ala Gly Val Thr Thr
145 150 155 160

Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg Pro Gly Gln Trp Ile Ala
165 170 175

Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu Ala Leu Gln Tyr Ala Lys
180 185 190

Asn Val Phe Asn Ala Lys Val Ile Ala Ile Asp Val Asn Asp Glu Gln
195 200 205

Leu Lys Leu Ala Thr Glu Met Gly Ala Asp Leu Ala Ile Asn Ser Arg
210 215 220

Thr Glu Asp Ala Ala Lys Ile Val Gln Glu Lys Thr Gly Gly Ala His
225 230 235 240

Ala Ala Val Val Thr Ala Val Ala Lys Ala Ala Phe Asn Ser Ala Val
245 250 255

Asp Ala Val Arg Ala Gly Gly Arg Val Val Ala Val Gly Leu Pro Pro
260 265 270

Glu Ser Met Ser Leu Asp Ile Pro Arg Leu Val Leu Asp Gly Ile Glu
275 280 285

Val Val Ser Ser Leu Val Gly Thr Arg Gln Asp Leu Thr Glu Ala Phe
290 295 300

Gln Phe Ala Ala Glu Gly Lys Val Val Pro Lys Val Ala Leu Arg Pro

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305 310 315 320

Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu Met Glu Glu Gly Lys Ile
325 330 335Arg Gly Arg Met Val Ile Asp Phe Arg Arg
340 345

<210> SEQ ID NO 59

<211> LENGTH: 346

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 59

Met Gln Asn Ile Ile Arg Lys Gly Gly Thr Met Lys Ala Ala Val Val
1 5 10 15Thr Lys Asp His His Val Asp Val Thr Asp Lys Thr Leu Arg Ser Leu
20 25 30Lys His Gly Glu Ala Leu Leu Lys Met Glu Cys Cys Gly Val Cys His
35 40 45Thr Asp Leu His Val Lys Asn Gly Asp Phe Gly Asp Lys Thr Gly Val
50 55 60Ile Leu Gly His Glu Gly Ile Gly Val Val Ala Glu Val Gly Pro Gly
65 70 75 80Val Thr Ser Leu Lys Pro Gly Asp Arg Ala Ser Val Ala Trp Phe Tyr
85 90 95Glu Gly Cys Gly His Cys Glu Tyr Cys Asn Ser Gly Asn Glu Thr Leu
100 105 110Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser Val Asp Gly Gly Met Ala
115 120 125Glu Glu Cys Ile Val Val Ala Asp Tyr Ala Val Lys Val Pro Asp Gly
130 135 140Leu Asp Ser Ala Ala Ala Ser Ser Ile Thr Cys Ala Gly Val Thr Thr
145 150 155 160Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg Pro Gly Gln Trp Ile Ala
165 170 175Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu Ala Leu Gln Tyr Ala Lys
180 185 190Asn Val Phe Asn Ala Lys Val Ile Ala Ile Asp Val Asn Asp Glu Gln
195 200 205Leu Lys Leu Ala Thr Glu Met Gly Ala Asp Leu Ala Ile Asn Ser Arg
210 215 220Thr Glu Asp Ala Ala Arg Ile Val Gln Glu Lys Ala Gly Gly Ala His
225 230 235 240Ala Ala Val Val Thr Ala Val Ala Lys Ala Ala Phe Asn Ser Ala Val
245 250 255Asp Ala Val Arg Ala Gly Gly Arg Val Val Ala Val Gly Leu Pro Pro
260 265 270Glu Ser Met Ser Leu Asp Ile Pro Arg Leu Val Leu Asp Gly Ile Glu
275 280 285Val Val Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Thr Glu Ala Phe
290 295 300Gln Phe Ala Ala Glu Gly Lys Val Val Pro Lys Val Ala Leu Arg Pro
305 310 315 320Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu Met Glu Glu Gly Lys Ile
325 330 335

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Arg Gly Arg Met Val Ile Asp Phe Arg Arg
340 345

<210> SEQ_ID NO 60
<211> LENGTH: 375
<212> TYPE: PRT
<213> ORGANISM: Shigella dysenteriae
<400> SEQUENCE: 60

Met Gln Asn Ile Ile Arg Lys Gly Gly Thr Met Lys Ala Ala Val Val
1 5 10 15

Thr Lys Asp His His Val Asp Val Thr Asp Lys Thr Leu Arg Ser Leu
20 25 30

Lys His Asp Glu Ala Leu Leu Lys Met Glu Cys Cys Gly Val Cys His
35 40 45

Thr Asp Leu His Val Lys Asn Gly Asp Phe Gly Asp Lys Thr Ser Val
50 55 60

Ile Leu Gly His Glu Gly Ile Gly Val Val Ala Glu Val Gly Pro Gly
65 70 75 80

Val Thr Ser Leu Lys Pro Gly Asp Arg Ala Ser Val Ala Trp Phe Tyr
85 90 95

Glu Gly Cys Gly His Cys Glu Tyr Cys Asn Ser Gly Asn Glu Thr Leu
100 105 110

Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser Val Asp Gly Gly Met Ala
115 120 125

Gln Glu Cys Ile Val Val Ala Asp Tyr Ala Val Lys Val Pro Asp Gly
130 135 140

Leu Asp Ser Ala Ala Ala Ser Ser Ile Thr Cys Ala Gly Val Thr Thr
145 150 155 160

Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg Pro Gly Gln Trp Ile Ala
165 170 175

Ile Tyr Gly Leu Gly Leu Gly Asn Leu Ala Leu Gln Tyr Ala Lys
180 185 190

Asn Val Phe Asn Ala Lys Val Ile Ala Ile Asp Val Asn Asp Glu Gln
195 200 205

Leu Lys Leu Ala Thr Glu Met Gly Ala Asp Leu Ala Ile Asn Ser Arg
210 215 220

Thr Glu Asp Ala Ala Lys Ile Val Gln Glu Lys Thr Gly Gly Ala His
225 230 235 240

Ala Ala Val Val Thr Ala Val Ala Lys Ala Ala Phe Asn Ser Ala Val
245 250 255

Asp Ala Val Arg Ala Gly Gly His Val Val Ala Val Gly Leu Pro Pro
260 265 270

Glu Ser Met Ser Leu Asp Ile Pro Arg Leu Val Leu Asp Gly Ile Glu
275 280 285

Val Val Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Thr Glu Ala Phe
290 295 300

Gln Phe Ala Ala Glu Gly Lys Val Val Pro Lys Val Ala Leu Arg Pro
305 310 315 320

Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu Met Glu Glu Gly Lys Ile
325 330 335

Arg Gly Arg Met Val Ile Asp Phe Arg Arg Ser Glu Ala Phe Ala Ala
340 345 350

Thr Ala Ser Pro Gly Val Ala Ala Ser His Thr Leu Gln His Glu Met
355 360 365

-continued

Ala Lys Trp Ile Ile Val Ala
370 375

<210> SEQ ID NO 61
<211> LENGTH: 336
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli
<400> SEQUENCE: 61

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Met Lys Ala Ala Val Val Thr Lys Asp His His Val Asp Val Thr Tyr
1           5          10          15

Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu
20          25          30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
35          40          45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
50          55          60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
65          70          75          80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
85          90          95

Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser
100         105         110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
115         120         125

Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
130         135         140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg
145         150         155         160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
165         170         175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
180         185         190

Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Glu Met Gly Ala Asp
195         200         205

Leu Ala Ile Asn Ser His Thr Glu Asp Ala Ala Lys Ile Val Gln Glu
210         215         220

Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
225         230         235         240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
245         250         255

Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu
260         265         270

Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln
275         280         285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
290         295         300

Lys Val Ala Leu Arg Pro Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu
305         310         315         320

Met Glu Glu Gly Lys Ile Arg Gly Arg Met Val Ile Asp Phe Arg His
325         330         335

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<210> SEQ ID NO 62
<211> LENGTH: 336
<212> TYPE: PRT

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-continued

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 62

Met Lys Ala Ala Val Val Thr Lys Asp His His Val Asp Val Thr Asp			
1	5	10	15

Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu		
20	25	30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe		
35	40	45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val		
50	55	60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala			
65	70	75	80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn		
85	90	95

Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser		
100	105	110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala		
115	120	125

Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr		
130	135	140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg			
145	150	155	160

Pro Gly Gln Trp Ile Ala Ile Tyr Glu Gly Gly Leu Gly Asn Leu		
165	170	175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile		
180	185	190

Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Glu Met Gly Ala Asp		
195	200	205

Leu Ala Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu		
210	215	220

Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala			
225	230	235	240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val		
245	250	255

Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu		
260	265	270

Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln		
275	280	285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro		
290	295	300

Lys Val Ala Leu Arg Pro Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu			
305	310	315	320

Met Glu Glu Gly Lys Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg		
325	330	335

<210> SEQ ID NO 63

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 63

Met Lys Ala Ala Val Val Thr Lys Asp His His Val Asp Val Thr Asp			
1	5	10	15

Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu		
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20 25 30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
 35 40 45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
 50 55 60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
 65 70 80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
 85 90 95

Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser
 100 105 110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
 115 120 125

Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Asn Ser Ile Thr
 130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg
 145 150 155 160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
 165 170 175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
 180 185 190

Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Glu Met Gly Ala Asp
 195 200 205

Leu Ala Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu
 210 215 220

Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
 225 230 235 240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
 245 250 255

Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu
 260 265 270

Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln
 275 280 285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
 290 295 300

Lys Val Ala Leu Arg Pro Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu
 305 310 315 320

Met Glu Glu Gly Lys Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg
 325 330 335

<210> SEQ ID NO 64

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Escherichia fergusonii

<400> SEQUENCE: 64

Met Lys Ala Ala Val Val Thr Lys Asp His His Val Asp Val Thr Asp
 1 5 10 15

Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu
 20 25 30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
 35 40 45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
 50 55 60

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Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
 65 70 75 80

 Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
 85 90 95

 Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser
 100 105 110

 Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
 115 120 125

 Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
 130 135 140

 Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg
 145 150 155 160

 Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
 165 170 175

 Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
 180 185 190

 Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Glu Ile Gly Ala Asp
 195 200 205

 Leu Ala Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu
 210 215 220

 Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
 225 230 235 240

 Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
 245 250 255

 Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu
 260 265 270

 Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln
 275 280 285

 Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
 290 295 300

 Lys Val Ala Leu Arg Pro Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu
 305 310 315 320

 Met Glu Glu Gly Lys Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg
 325 330 335

<210> SEQ ID NO 65

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 65

Met Lys Ala Ala Val Val Thr Lys Asp His His Val Asp Val Thr Asp
 1 5 10 15

 Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu
 20 25 30

 Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
 35 40 45

 Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
 50 55 60

 Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
 65 70 75 80

 Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
 85 90 95

 Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser
 100 105 110

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Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
115 120 125

Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg
145 150 155 160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
165 170 175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
180 185 190

Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Glu Met Gly Ala Asp
195 200 205

Leu Ala Ile Asn Ser Arg Thr Glu Asp Ala Ala Arg Ile Val Gln Glu
210 215 220

Lys Ala Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
225 230 235 240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
245 250 255

Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu
260 265 270

Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln
275 280 285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
290 295 300

Lys Val Ala Leu Arg Pro Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu
305 310 315 320

Met Glu Glu Gly Lys Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg
325 330 335

<210> SEQ ID NO 66
<211> LENGTH: 336
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 66

Met Lys Ala Ala Val Val Thr Lys Asp His His Val Asp Val Thr Asp
1 5 10 15

Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu
20 25 30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
35 40 45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
50 55 60

Ala Glu Val Gly Ser Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
65 70 75 80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
85 90 95

Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser
100 105 110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
115 120 125

Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg

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145	150	155	160
Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu			
165	170	175	
Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile			
180	185	190	
Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Glu Met Gly Ala Asp			
195	200	205	
Leu Ala Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu			
210	215	220	
Lys Thr Ser Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala			
225	230	235	240
Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val			
245	250	255	
Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu			
260	265	270	
Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln			
275	280	285	
Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro			
290	295	300	
Lys Val Ala Leu Arg Pro Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu			
305	310	315	320
Met Glu Glu Gly Lys Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg			
325	330	335	

<210> SEQ ID NO: 67

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Shigella flexneri

<400> SEQUENCE: 67

Met Lys Thr Ala Val Val Thr Lys Asp His His Val Asp Val Thr Asp			
1	5	10	15
Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu			
20	25	30	
Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe			
35	40	45	
Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val			
50	55	60	
Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala			
65	70	75	80
Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn			
85	90	95	
Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser			
100	105	110	
Val Asp Gly Gly Met Glu Glu Glu Cys Ile Val Val Ala Asp Tyr Ala			
115	120	125	
Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Pro Ser Ser Ile Thr			
130	135	140	
Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg			
145	150	155	160
Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu			
165	170	175	
Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile			
180	185	190	

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Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Glu Met Asp Ala Asp
195 200 205

Leu Ala Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu
210 215 220

Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
225 230 235 240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
245 250 255

Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu
260 265 270

Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln
275 280 285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
290 295 300

Lys Val Ala Leu Arg Pro Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu
305 310 315 320

Met Glu Glu Gly Lys Ile Arg Gly Arg Met Val Ile Asp Phe Arg His
325 330 335

<210> SEQ ID NO 68

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 68

Met Lys Ala Ala Val Val Thr Lys Asp His His Val Asp Val Thr Asp
1 5 10 15

Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu
20 25 30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
35 40 45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
50 55 60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
65 70 75 80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
85 90 95

Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser
100 105 110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
115 120 125

Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg
145 150 155 160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
165 170 175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
180 185 190

Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Glu Met Gly Ala Asp
195 200 205

Leu Ala Ile Asn Ser Arg Thr Glu Asp Ala Ala Arg Ile Val Gln Glu
210 215 220

Lys Ala Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
225 230 235 240

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Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
245 250 255

Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu
260 265 270

Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln
275 280 285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
290 295 300

Lys Val Ala Leu Arg Pro Leu Glu Asp Ile Asn Thr Ile Phe Thr Glu
305 310 315 320

Met Glu Glu Gly Lys Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg
325 330 335

<210> SEQ ID NO 69

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 69

Met Lys Ala Ala Val Val Thr Lys Asp His His Val Asp Val Thr Asp
1 5 10 15

Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu
20 25 30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
35 40 45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
50 55 60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
65 70 75 80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
85 90 95

Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser
100 105 110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
115 120 125

Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg
145 150 155 160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
165 170 175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
180 185 190

Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Lys Met Gly Ala Asp
195 200 205

Leu Ala Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu
210 215 220

Lys Ala Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
225 230 235 240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
245 250 255

Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu
260 265 270

Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln

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275 280 285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
 290 295 300

Lys Val Ala Leu Arg Pro Leu Glu Asp Ile Asn Thr Ile Phe Thr Glu
 305 310 315 320

Met Glu Glu Gly Lys Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg
 325 330 335

<210> SEQ ID NO 70

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 70

Met Lys Ala Ala Val Val Thr Lys Ala His His Val Asp Val Thr Asp
 1 5 10 15

Lys Thr Leu Arg Ser Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu
 20 25 30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
 35 40 45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
 50 55 60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
 65 70 75 80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
 85 90 95

Ser Gly Asn Glu Thr Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser
 100 105 110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
 115 120 125

Val Lys Val Pro Asp Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
 130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Leu Ser Lys Ile Arg
 145 150 155 160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
 165 170 175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
 180 185 190

Asp Val Asn Asp Glu Gln Leu Lys Leu Ala Thr Glu Met Gly Ala Asp
 195 200 205

Leu Ala Ile Asn Ser Arg Thr Glu Asp Ala Ala Arg Ile Val Gln Glu
 210 215 220

Lys Ala Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
 225 230 235 240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
 245 250 255

Ala Val Gly Leu Pro Pro Glu Ser Met Ser Leu Asp Ile Pro Arg Leu
 260 265 270

Val Leu Asp Gly Ile Glu Val Val Gly Ser Leu Val Gly Thr Arg Gln
 275 280 285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
 290 295 300

Lys Val Ala Leu Arg Pro Leu Ala Asp Ile Asn Thr Ile Phe Thr Glu
 305 310 315 320

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Met	Glu	Glu	Gly	Lys	Ile	Arg	Gly	Arg	Met	Val	Ile	Asp	Phe	Arg	Arg
									325	330					335

<210> SEQ ID NO 71

<211> LENGTH: 365

<212> TYPE: PRT

<213> ORGANISM: Shigella dysentariae

<400> SEQUENCE: 71

Met	Lys	Ala	Ala	Val	Val	Thr	Lys	Asp	His	His	Val	Asp	Val	Thr	Asp
									5	10		15			

Lys	Thr	Leu	Arg	Ser	Leu	Lys	His	Asp	Glu	Ala	Leu	Leu	Lys	Met	Glu
									20	25		30			

Cys	Cys	Gly	Val	Cys	His	Thr	Asp	Leu	His	Val	Lys	Asn	Gly	Asp	Phe
									35	40		45			

Gly	Asp	Lys	Thr	Ser	Val	Ile	Leu	Gly	His	Glu	Gly	Ile	Gly	Val	Val
									50	55		60			

Ala	Glu	Val	Gly	Pro	Gly	Val	Thr	Ser	Leu	Lys	Pro	Gly	Asp	Arg	Ala
									65	70		75		80	

Ser	Val	Ala	Trp	Phe	Tyr	Glu	Gly	Cys	Gly	His	Cys	Glu	Tyr	Cys	Asn
									85	90		95			

Ser	Gly	Asn	Glu	Thr	Leu	Cys	Arg	Ser	Val	Lys	Asn	Ala	Gly	Tyr	Ser
									100	105		110			

Val	Asp	Gly	Gly	Met	Ala	Gln	Glu	Cys	Ile	Val	Val	Ala	Asp	Tyr	Ala
									115	120		125			

Val	Lys	Val	Pro	Asp	Gly	Leu	Asp	Ser	Ala	Ala	Ser	Ser	Ile	Thr	
									130	135		140			

Cys	Ala	Gly	Val	Thr	Thr	Tyr	Lys	Ala	Val	Lys	Leu	Ser	Lys	Ile	Arg
									145	150		155		160	

Pro	Gly	Gln	Trp	Ile	Ala	Ile	Tyr	Gly	Leu	Gly	Gly	Leu	Gly	Asn	Leu
									165	170		175			

Ala	Leu	Gln	Tyr	Ala	Lys	Asn	Val	Phe	Asn	Ala	Lys	Val	Ile	Ala	Ile
									180	185		190			

Asp	Val	Asn	Asp	Glu	Gln	Leu	Lys	Leu	Ala	Thr	Glu	Met	Gly	Ala	Asp
									195	200		205			

Leu	Ala	Ile	Asn	Ser	Arg	Thr	Glu	Asp	Ala	Ala	Lys	Ile	Val	Gln	Glu
									210	215		220			

Lys	Thr	Gly	Gly	Ala	His	Ala	Ala	Val	Val	Thr	Ala	Val	Ala	Lys	Ala
									225	230		235		240	

Ala	Phe	Asn	Ser	Ala	Val	Asp	Ala	Val	Arg	Ala	Gly	Gly	His	Val	Val
									245	250		255			

Ala	Val	Gly	Leu	Pro	Pro	Glu	Ser	Met	Ser	Leu	Asp	Ile	Pro	Arg	Leu
									260	265		270			

Val	Leu	Asp	Gly	Ile	Glu	Val	Val	Gly	Ser	Leu	Val	Gly	Thr	Arg	Gln
									275	280		285			

Asp	Leu	Thr	Glu	Ala	Phe	Gln	Phe	Ala	Ala	Glu	Gly	Lys	Val	Val	Pro
									290	295		300			

Lys	Val	Ala	Leu	Arg	Pro	Leu	Ala	Asp	Ile	Asn	Thr	Ile	Phe	Thr	Glu
									305	310		315		320	

Met	Glu	Gly	Lys	Ile	Arg	Gly	Arg	Met	Val	Ile	Asp	Phe	Arg	Arg	
									325	330		335			

Ser	Glu	Ala	Phe	Ala	Ala	Thr	Ala	Ser	Pro	Gly	Val	Ala	Ala	Ser	His
									340	345		350			

Thr	Leu	Gln	His	Glu	Met	Ala	Lys	Trp	Ile	Ile	Val	Ala			
									355	360		365			

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<210> SEQ_ID NO 72
 <211> LENGTH: 336
 <212> TYPE: PRT
 <213> ORGANISM: *Salmonella enterica*
 <400> SEQUENCE: 72

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Met Lys Ala Ala Val Val Thr Gln Asp His Gln Val Asp Val Thr Glu
  1           5          10          15

Lys Thr Leu Arg Pro Leu Arg His Gly Glu Ala Leu Leu Lys Met Glu
  20          25          30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
  35          40          45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
  50          55          60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
  65          70          75          80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
  85          90          95

Thr Gly Asn Glu Thr Leu Cys Arg Asn Val Lys Asn Ala Gly Tyr Thr
  100         105         110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
  115         120         125

Val Lys Val Pro Glu Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
  130         135         140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Ile Ser His Ile Lys
  145         150         155         160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
  165         170         175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
  180         185         190

Asp Val Asn Asp Gly Gln Leu Lys Leu Ala Glu Glu Met Gly Ala Asp
  195         200         205

Leu Thr Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu
  210         215         220

Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
  225         230         235         240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
  245         250         255

Ala Val Gly Leu Pro Pro Glu Ala Met Asn Leu Asp Ile Pro Arg Leu
  260         265         270

Val Leu Asp Gly Ile Gln Val Val Gly Ser Leu Val Gly Thr Arg Gln
  275         280         285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
  290         295         300

Lys Val Ala Leu Arg Pro Leu Glu Asp Ile Asn Val Ile Phe Lys Glu
  305         310         315         320

Met Glu Gln Gly Gln Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg
  325         330         335
  
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<210> SEQ_ID NO 73
 <211> LENGTH: 336
 <212> TYPE: PRT
 <213> ORGANISM: *Salmonella enterica*
 <400> SEQUENCE: 73

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Met Lys Ala Ala Val Val Thr Gln Asp His Gln Val Asp Val Thr Glu
 1 5 10 15
 Lys Thr Leu Arg Pro Leu Arg His Gly Glu Ala Leu Leu Lys Met Glu
 20 25 30
 Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
 35 40 45
 Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
 50 55 60
 Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
 65 70 75 80
 Ser Val Ala Trp Phe Tyr Glu Gly Cys His Cys Glu Tyr Cys Asn
 85 90 95
 Thr Gly Asn Glu Thr Leu Cys Arg Asn Val Lys Asn Ala Gly Tyr Thr
 100 105 110
 Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
 115 120 125
 Val Lys Val Pro Glu Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
 130 135 140
 Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Ile Ser His Ile Lys
 145 150 155 160
 Pro Gly Gln Trp Ile Ala Ile Tyr Glu Gly Leu Gly Leu Gly Asn Leu
 165 170 175
 Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
 180 185 190
 Asp Val Asn Asp Gly Gln Leu Lys Leu Ala Glu Glu Met Gly Ala Asp
 195 200 205
 Leu Thr Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu
 210 215 220
 Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
 225 230 235 240
 Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
 245 250 255
 Ala Val Gly Leu Pro Pro Glu Ala Met Asn Leu Asp Ile Pro Arg Leu
 260 265 270
 Val Leu Asp Gly Ile Gln Val Val Gly Ser Leu Val Gly Thr Arg Gln
 275 280 285
 Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
 290 295 300
 Lys Val Ala Leu Arg Pro Leu Glu Asp Ile Asn Ala Ile Phe Lys Glu
 305 310 315 320
 Met Glu Gln Gly Gln Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg
 325 330 335

<210> SEQ ID NO 74
 <211> LENGTH: 336
 <212> TYPE: PRT
 <213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 74

Met Lys Ala Val Val Val Thr Gln Asp His Gln Val Asp Val Thr Glu
 1 5 10 15
 Lys Thr Leu Arg Pro Leu Arg His Gly Glu Ala Leu Leu Lys Met Glu
 20 25 30
 Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe

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35	40	45
Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val		
50	55	60
Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala		
65	70	75
80		
Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn		
85	90	95
Thr Gly Asn Glu Thr Leu Cys Arg Asn Val Lys Asn Ala Gly Tyr Thr		
100	105	110
Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala		
115	120	125
Val Lys Val Pro Glu Gly Leu Asp Ser Ala Ala Ala Ser Ser Ile Thr		
130	135	140
Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Ile Ser His Ile Lys		
145	150	155
160		
Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu		
165	170	175
Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile		
180	185	190
Asp Val Asn Asp Gly Gln Leu Lys Leu Ala Glu Glu Met Gly Ala Asp		
195	200	205
Leu Thr Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu		
210	215	220
Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala		
225	230	235
240		
Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val		
245	250	255
Ala Val Gly Leu Pro Pro Glu Ala Met Asn Leu Asp Ile Pro Arg Leu		
260	265	270
Val Leu Asp Gly Ile Gln Val Val Gly Ser Leu Val Gly Thr Arg Gln		
275	280	285
Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro		
290	295	300
Lys Val Ala Leu Arg Pro Leu Glu Asp Ile Asn Val Ile Phe Lys Glu		
305	310	315
320		
Met Glu Gln Gly Gln Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg		
325	330	335

<210> SEQ ID NO 75
<211> LENGTH: 336
<212> TYPE: PRT
<213> ORGANISM: *Salmonella enterica*

<400> SEQUENCE: 75

Lys Thr Leu Arg Pro Leu Arg His Gly Glu Ala Leu Leu Lys Met Glu
20 25 30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
35 40 45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
50 55 60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
65 70 75 80

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Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
85 90 95

Thr Gly Asn Glu Thr Leu Cys Arg Asn Val Lys Asn Ala Gly Tyr Thr
100 105 110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
115 120 125

Val Lys Val Pro Glu Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
130 135 140

Cys Ala Gly Val Ala Thr Tyr Lys Ala Val Lys Ile Ser His Ile Lys
145 150 155 160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
165 170 175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
180 185 190

Asp Val Asn Asp Gly Gln Leu Lys Leu Ala Glu Glu Met Gly Ala Asp
195 200 205

Leu Thr Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu
210 215 220

Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
225 230 235 240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
245 250 255

Ala Val Gly Leu Pro Pro Glu Ala Met Asn Leu Asp Ile Pro Arg Leu
260 265 270

Val Leu Asp Gly Ile Gln Val Val Gly Ser Leu Val Gly Thr Arg Gln
275 280 285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
290 295 300

Lys Val Ala Leu Arg Pro Leu Glu Asp Ile Asn Val Ile Phe Lys Glu
305 310 315 320

Met Glu Gln Gly Gln Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg
325 330 335

<210> SEQ ID NO 76

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 76

Met Lys Ala Ala Val Val Thr Gln Asp His Gln Val Asp Val Thr Glu
1 5 10 15

Lys Thr Leu Arg Pro Leu Arg His Gly Glu Ala Leu Leu Lys Met Glu
20 25 30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
35 40 45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
50 55 60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
65 70 75 80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu His Cys Asn
85 90 95

Thr Gly Asn Glu Thr Leu Cys Arg Asn Val Lys Asn Ala Gly Tyr Thr
100 105 110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
115 120 125

-continued

Val Lys Val Pro Glu Gly Leu Asp Ser Ala Ala Ala Ser Ser Ile Thr
130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Ile Ser His Ile Lys
145 150 155 160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu
165 170 175

Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile
180 185 190

Asp Val Asn Asp Gly Gln Leu Lys Leu Ala Glu Glu Met Gly Ala Asp
195 200 205

Leu Thr Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu
210 215 220

Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala
225 230 235 240

Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val
245 250 255

Ala Val Gly Leu Pro Pro Glu Ala Met Asn Leu Asp Ile Pro Arg Leu
260 265 270

Val Leu Asp Gly Ile Gln Val Val Gly Ser Leu Val Gly Thr Arg Gln
275 280 285

Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro
290 295 300

Lys Val Ala Leu Arg Pro Leu Glu Asp Ile Asn Val Ile Phe Lys Glu
305 310 315 320

Met Glu Gln Gly Gln Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg
325 330 335

<210> SEQ ID NO 77

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 77

Met Lys Ala Ala Val Val Thr Gln Asp His Gln Val Asp Val Thr Glu
1 5 10 15

Lys Thr Leu Arg Pro Leu Arg His Gly Glu Ala Leu Leu Lys Met Glu
20 25 30

Cys Cys Gly Val Cys His Thr Asp Leu His Val Lys Asn Gly Asp Phe
35 40 45

Gly Asp Lys Thr Gly Val Ile Leu Gly His Glu Gly Ile Gly Val Val
50 55 60

Ala Glu Val Gly Pro Gly Val Thr Ser Leu Lys Pro Gly Asp Arg Ala
65 70 75 80

Ser Val Ala Trp Phe Tyr Glu Gly Cys Gly His Cys Glu Tyr Cys Asn
85 90 95

Thr Gly Asn Glu Thr Leu Cys Cys Asn Val Lys Asn Ala Gly Tyr Thr
100 105 110

Val Asp Gly Gly Met Ala Glu Glu Cys Ile Val Val Ala Asp Tyr Ala
115 120 125

Val Lys Val Pro Glu Gly Leu Asp Ser Ala Ala Ser Ser Ile Thr
130 135 140

Cys Ala Gly Val Thr Thr Tyr Lys Ala Val Lys Ile Ser His Ile Lys
145 150 155 160

Pro Gly Gln Trp Ile Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu

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165	170	175
Ala Leu Gln Tyr Ala Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile		
180	185	190
Asp Val Asn Asp Gly Gln Leu Lys Leu Ala Glu Glu Met Gly Ala Asp		
195	200	205
Leu Thr Ile Asn Ser Arg Thr Glu Asp Ala Ala Lys Ile Val Gln Glu		
210	215	220
Lys Thr Gly Gly Ala His Ala Ala Val Val Thr Ala Val Ala Lys Ala		
225	230	235
240		
Ala Phe Asn Ser Ala Val Asp Ala Val Arg Ala Gly Gly Arg Val Val		
245	250	255
Ala Val Gly Leu Pro Pro Glu Ala Met Asn Leu Asp Ile Pro Arg Leu		
260	265	270
Val Leu Asp Gly Ile Gln Val Val Gly Ser Leu Val Gly Thr Arg Gln		
275	280	285
Asp Leu Thr Glu Ala Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro		
290	295	300
Lys Val Ala Leu Arg Pro Leu Glu Asp Ile Asn Val Ile Phe Lys Glu		
305	310	315
320		
Met Glu Gln Gly Gln Ile Arg Gly Arg Met Val Ile Asp Phe Arg Arg		
325	330	335

<210> SEQ ID NO 78

<211> LENGTH: 347

<212> TYPE: PRT

<213> ORGANISM: Enterobacter cancerogenus

<400> SEQUENCE: 78

Met Gln Met His Ile Met Asn Lys Glu Lys Gln Met Lys Ala Ala Val		
1	5	10
15		
Val Thr Gln Asp His Gln Val Asn Val Thr Glu Lys Thr Leu Arg Pro		
20	25	30
Leu Lys His Gly Glu Ala Leu Leu Lys Met Glu Cys Cys Gly Val Cys		
35	40	45
His Thr Asp Leu His Val Lys Asn Gly Asp Phe Gly Asp Lys Thr Gly		
50	55	60
Val Ile Leu Gly His Glu Gly Ile Gly Ile Val Lys Glu Ile Gly Pro		
65	70	75
80		
Gly Val Asn Ser Leu Lys Val Gly Asp Arg Ala Ser Val Ala Trp Phe		
85	90	95
Phe Glu Gly Cys Gly His Cys Glu Tyr Cys Asn Ala Gly Asn Glu Thr		
100	105	110
Leu Cys Arg Ser Val Lys Asn Ala Gly Tyr Ser Val Asp Gly Gly Met		
115	120	125
Ala Glu Glu Cys Ile Val Thr Ala Asp Tyr Ala Val Lys Val Pro Asp		
130	135	140
Gly Leu Gly Ser Ala Ala Ser Ser Ile Thr Cys Ala Gly Val Thr		
145	150	155
160		
Thr Tyr Lys Ala Val Lys Ile Ser Thr Ile Lys Pro Gly Gln Trp Ile		
165	170	175
Ala Ile Tyr Gly Leu Gly Gly Leu Gly Asn Leu Ala Leu Gln Tyr Ala		
180	185	190
Lys Asn Val Phe Asn Ala Lys Val Ile Ala Ile Asp Val Asn Asp Glu		
195	200	205

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Gln Leu Lys Leu Ala Ala Ser Met Gly Ala Asp Leu Thr Ile Asn Ser
 210 215 220

 Arg Asn Glu Asp Ala Ala Lys Val Ile Gln Glu Lys Thr Gly Gly Ala
 225 230 235 240

 His Ala Ala Val Val Thr Ala Val Ala Lys Ala Ala Phe Asn Ser Ala
 245 250 255

 Val Asp Ala Val Arg Ala Gly Gly Arg Val Val Ala Val Gly Leu Pro
 260 265 270

 Pro Glu Ala Met Ser Leu Asp Ile Pro Arg Leu Val Leu Asp Gly Ile
 275 280 285

 Gln Val Val Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Val Glu Ala
 290 295 300

 Phe Gln Phe Ala Ala Glu Gly Lys Val Val Pro Lys Val Thr Met Arg
 305 310 315 320

 Pro Leu Glu Asp Ile Asn Ala Ile Phe Lys Glu Met Glu Gln Gly Gln
 325 330 335

 Ile Arg Gly Arg Met Val Ile Asp Leu Arg Ala
 340 345

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The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1. A recombinant prokaryotic microorganism metabolically engineered from a parental prokaryotic microorganism to produce 1,4-butanediol, said recombinant prokaryotic microorganism comprising genes encoding the following:

a. a xylonate dehydrogenase that catalyzes the conversion of xylose to xylonic acid, wherein said xylonate dehydrogenase comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 2 or to the amino acid sequence of SEQ ID NO: 4;

b. a xylonate dehydratase that catalyzes the conversion of xylonic acid to 3-deoxy-D-glycero-pentulosonic acid, wherein said xylonate dehydratase comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 6 or to the amino acid sequence of SEQ ID NO: 8;

amino acid sequence of SEQ ID NO: 8;

c. a decarboxylase that catalyzes conversion of 3-deoxy-D-glycero-pentulosonic acid to 3,4-dihydroxy-D-butanal, wherein said decarboxylase comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 9;

d. a first alcohol dehydrogenase that catalyzes conversion of 3,4-dihydroxy-D-butanal to 1,2,4-butanetriol, wherein said first alcohol dehydrogenase comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO:10;

e. a diol dehydratase that catalyzes conversion of 1,2,4-butanetriol to 4-hydroxybutanal, wherein said diol dehydratase is selected from the group consisting of GIIdABC from *Klebsiella*, PddABC from *Klebsiella*, or DhaB123 from *Clostridium*; and

f. a second alcohol dehydrogenase that catalyzes conversion of 4-hydroxybutanal to 1,4-butanediol, wherein said second alcohol dehydrogenase comprises an amino acid sequence having at least 90% sequence identity to the amino acid sequence of SEQ ID NO: 10; wherein at least one of the genes encoding said xylonate dehydrogenase, said xylonate dehydratase, said decarboxylase, said first alcohol dehydrogenase, said diol dehydratase,

and said second alcohol dehydrogenase is heterologous to said recombinant prokaryotic microorganism and is associated with a heterologous expression control sequence resulting in the overexpression thereof.

2. The recombinant prokaryotic microorganism of claim 1, wherein the microorganism over-expresses one or more of the xylonate dehydrogenase, the xylonate dehydratase, the decarboxylase, the first alcohol dehydrogenase, the diol dehydratase, and the second alcohol dehydrogenase, as compared to the parental microorganism.

3. The recombinant prokaryotic microorganism of claim 1, wherein said gene encoding the xylonate dehydrogenase is heterologous to the parental microorganism.

4. The recombinant prokaryotic microorganism of claim 1, wherein said xylonate dehydrogenase comprises the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4.

5. The recombinant prokaryotic microorganism of claim 1, wherein said gene encoding said xylonate dehydratase is heterologous to the parental microorganism.

6. The recombinant prokaryotic microorganism of claim 1, wherein said xylonate dehydratase is a heterologous D-xylose dehydratase comprising the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8.

7. The recombinant prokaryotic microorganism of claim 1, wherein said gene encoding said decarboxylase is heterologous to the parental microorganism.

8. The recombinant prokaryotic microorganism of claim 1, wherein said decarboxylase is a heterologous decarboxylase comprising the amino acid sequence of SEQ ID NO:9.

9. The recombinant prokaryotic microorganism of claim 1, wherein said gene encoding said first alcohol dehydrogenase or said gene encoding said second alcohol dehydrogenase is heterologous to the parental microorganism.

10. The recombinant prokaryotic microorganism of claim 9, wherein said first alcohol dehydrogenase or said second alcohol dehydrogenase comprises the amino acid sequence of SEQ ID NO: 10.

11. The recombinant prokaryotic microorganism of claim 1, wherein said first alcohol dehydrogenase is the same as said second alcohol dehydrogenase.

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12. The recombinant prokaryotic microorganism of claim 1, wherein said first alcohol dehydrogenase is different from said second alcohol dehydrogenase.

13. The recombinant prokaryotic microorganism of claim 1, wherein said microorganism further reduces expression of a polypeptide compared to the expression of said polypeptide in the parental prokaryotic organism, wherein said polypeptide produces a flux in the parental prokaryotic organism that competes with one or more metabolic intermediates for the production of 1,4-butanediol, wherein said polypeptide is selected from the group consisting of a D-xylose isomerase, a 2-keto acid aldolase, a 2-keto acid transaminase, a 2-keto acid dehydrogenase, and any combination thereof. 5

14. The recombinant prokaryotic microorganism of claim 1, wherein said microorganism is selected from *Escherichia*, ¹⁵ *Corynebacterium*, *Lactobacillus*, and *Bacillus*.

15. The recombinant prokaryotic microorganism of claim 14, wherein said microorganism is *Escherichia coli*.

16. A method of producing 1,4-butanediol, comprising:
a. providing the recombinant prokaryotic microorganism of claim 1;
b. culturing said recombinant prokaryotic microorganism in the presence of xylose under conditions suitable for the conversion of xylose to 1,4-butanediol; and
c. isolating the 1,4-butanediol. 25

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